OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 13, 2005, 02:43:55

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI...........SLSAVVFGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 41601S017 residues

Total number of hits satisfying chosen parameters: 1854112

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

; Search time 110.575 Seconds
(without alignments)
428.900 Million cell updates//sec

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.3	114	14	US-10-010-729-9	Sequence 9, Appli
2	539	92.0	234	14	US-10-194-801C-4	Sequence 4, Appli
3	539	92.0	248	15	US-10-779-461-50	Sequence 50, Appl
4	538	91.8	243	14	US-10-322-673-53	Sequence 53, Appl
5	538	91.8	243	18	US-10-981-465-53	Sequence 53, Appl
6	538	91.8	243	18	US-10-981-621-53	Sequence 53, Appl
7	538	91.8	243	18	US-10-981-673-53	Sequence 53, Appl
8	538	91.8	243	18	US-10-981-691-53	Sequence 53, Appl
9	537	91.6	110	17	US-10-727-155-309	Sequence 309, App
10	537	91.6	110	17	US-10-727-155-311	Sequence 311, App
11	534	91.1	258	10	US-09-880-748-1260	Sequence 1260, Ap
12	534	91.1	258	15	US-10-293-418-1260	Sequence 1260, Ap
13	533	91.0	234	10	US-09-880-748-1246	Sequence 1246, Ap
14	533	91.0	248	15	US-10-293-418-1246	Sequence 1246, Ap
15	532	90.8	112	14	US-10-269-805-10	Sequence 10, Ap
16	530	90.4	255	15	US-09-880-748-1156	Sequence 1156, Ap
17	530	90.4	255	15	US-10-293-418-1156	Sequence 1156, Ap
18	528	90.1	110	17	US-10-727-155-86	Sequence 86, Appl
19	528	90.1	110	17	US-10-727-155-164	Sequence 164, Appl
20	528	90.1	248	16	US-09-880-748-861	Sequence 861, Appl
21	528	90.1	248	16	US-10-293-418-861	Sequence 861, Appl
22	528	90.1	248	15	US-10-779-461-21	Sequence 21, Appl
23	528	90.1	251	15	US-09-880-748-1551	Sequence 1551, Ap
24	528	90.1	251	15	US-10-293-418-1551	Sequence 1551, Ap
25	527.5	90.0	111	14	US-09-880-748-1859	Sequence 1859, Ap
26	526	89.8	253	10	US-10-935-290-127	Sequence 127, App
27	526	89.8	251	17	US-10-779-461-4	Sequence 4, Appli
28	523	89.2	244	16	US-09-880-748-1465	Sequence 1465, Ap
29	522	89.1	251	17	US-10-293-418-1465	Sequence 1465, Ap
30	522	89.1	248	16	US-09-880-748-25	Sequence 25, Appl
31	522	89.1	248	15	US-10-293-418-1538	Sequence 1538, Ap
32	522	89.1	251	15	US-10-981-692-25	Sequence 25, Appl
33	522	89.1	251	18	US-09-880-748-1538	Sequence 1538, Ap
34	522	89.1	256	10	US-10-293-418-1015	Sequence 1015, Ap
35	522	89.1	256	10	US-09-880-748-1015	Sequence 1015, Ap
36	521	88.9	123	14	US-10-293-416-53	Sequence 53, Appl
37	521	88.9	123	14	US-10-153-437-6	Sequence 6, Appli
38	521	88.9	130	18	US-10-909-851-28	Sequence 28, Appl
39	520	88.7	248	16	US-11-090-847-111	Sequence 111, Ap
40	520	88.6	248	20	US-09-880-748-1139	Sequence 1139, Ap
41	519	88.6	254	15	US-09-880-748-1139	Sequence 1139, Ap
42	519	88.6	254	15	US-10-293-418-1139	Sequence 1139, Ap
43	519	88.6	255	15	US-10-779-461-53	Sequence 53, Appl
44	519	88.6	255	15	US-09-293-418-857	Sequence 857, App
45	518	88.4	110	15	US-10-440-522-7	Sequence 7, Appli

RESULT 1

US-10-010-729-9

; Sequence 9, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-729-9

ALIGNMENTS

; Sequence 50, Application US/10779461
; Publication No. US20040166544A1
; GENERAL INFORMATION:
; APPLICANT: Morton, Philip A
; TITLE OF INVENTION: ANTIBODIES TO c-MET FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 00980/1
; CURRENT APPLICATION NUMBER: US/10/779,461
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,073
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 50
; LENGTH: 248
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: phage display generated human antibody
US-10-779-461-50

  Query Match   92.0%; Score 539; DB 16; Length 248;
  Best Local Similarity   98.3%; Pred. No. 2.9e-42;
  Matches 103; Conservative   3; Mismatches   5; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
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Db   138 QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPRLLIYDNNKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG 111
            ||||||||||||||||||||||||||||||||:|:||||||||||||||||
Db   198 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGGVFGGGTKLTVLG 248

RESULT 4
US-10-322-673-53
; Sequence 53, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo   et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
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; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-322-673-53

  Query Match   91.8%; Score 538; DB 14; Length 243;
  Best Local Similarity   91.9%; Pred. No. 3.5e-42;
  Matches 102; Conservative   5; Mismatches   4; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
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Db   133 QSVITQPPSVSAAPGQKVTISCSGSGTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

RESULT 2
US-10-194-801C-4
; Sequence 4, Application US/10194801C
; Publication No. US20030143643A1
; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
;   Ramon Montano
; TITLE OF INVENTION: Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Shapiro & Dupont LLP
; STREET: 233 Wilshire Boulevard, Suite 700
; CITY: Santa Monica
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/194,801C
; FILING DATE: 11-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/372,425
; FILING DATE: August 11, 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 0180.0033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 319-5411
; TELEFAX: (310) 319-5401
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Light chain - AA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-10-194-801C-4

  Query Match   92.0%; Score 539; DB 14; Length 234;
  Best Local Similarity   89.5%; Pred. No. 2.7e-42;
  Matches 102; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
            ||||:|||||:||||||||||||:|||||||:||||::||::|||||||||:|||||||
Db   19 QSVLTQPPSVSAAPGKVTISCSGSSSNIGNNYVSWYQHPGTAPKLLTVLGQPK 78

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQPK 114
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Db   79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNSSLSAVLFGGGTEVTVLGQPK 132

RESULT 3
US-10-779-461-50

Query Match   99.3%; Score 582; DB 14; Length 114;
Best Local Similarity   98.2%; Pred. No. 1.3e-46;
Matches 112; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPRLLIYDITKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQPK 114
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQPK 114

RESULT 3
US-10-779-461-50

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Qy    61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||| ||||||||||| |||||||| ||||
Db   193  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243
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RESULT 5
US-10-981-465-53
Sequence 53, Application US/10981465
Publication No. US20050214205A1
GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1
; CURRENT APPLICATION NUMBER: US/10/981,465
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-981-465-53

Query Match   91.8%; Score 538; DB 18;   Length 243;
Best Local Similarity   91.9%; Pred. No. 3.5e-42;
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Db   133  QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy    61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||| ||||||||||| |||||||| ||||
Db   193  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243
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RESULT 6
US-10-981-621-53
Sequence 53, Application US/10981621
Publication No. US20050214206A1
GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D1
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900

; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-981-621-53

Query Match   91.8%; Score 538; DB 18;   Length 243;
Best Local Similarity   91.9%; Pred. No. 3.5e-42;
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||:||||||||||| ||||||||| ||||||||||||||
Db   133  QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy    61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||| ||||||||||| |||||||| ||||
Db   193  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243
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RESULT 7
US-10-981-673-53
Sequence 53, Application US/10981673
Publication No. US20050214207A1
GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585P1D2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76

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;  SEQ ID NO 53
;    LENGTH: 243
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: CM085C11 scFv
US-10-981-673-53

  Query Match             91.8%;  Score 538;  DB 18;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 3.5e-42;
  Matches 102;  Conservative   5;  Mismatches   4;  Indels   0;  Gaps   0;

Qy      1  QSVLTQPPSVSAAPGQKVTISCSGSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db    133  QSVLTQPPSVSAAPGQKVTISCSGSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy     61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
           |||||||||||||||||||||||| :|||||||||||||||| :||||
Db    193  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243
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RESULT 8
US-10-981-691-53
; Sequence 53, Application US/10981691
; Publication No. US20050214208A1
; GENERAL INFORMATION:
;    APPLICANT: Salcedo et al.
;    TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;    TITLE OF INVENTION: Receptors
;    FILE REFERENCE: PF585PID3
; CURRENT APPLICATION NUMBER: US/10/981,691
; CURRENT FILING DATE:
;    PRIOR APPLICATION NUMBER: 2004-11-05
;    PRIOR APPLICATION NUMBER: 60/608,386
;    PRIOR FILING DATE: 2004-09-10
;    PRIOR APPLICATION NUMBER: PCT/US04/013900
;    PRIOR FILING DATE:
;    PRIOR APPLICATION NUMBER: 60/468,092
;    PRIOR FILING DATE: 2003-05-06
;    PRIOR APPLICATION NUMBER: 60/495,140
;    PRIOR FILING DATE: 2003-08-15
;    PRIOR APPLICATION NUMBER: 10/322,673
;    PRIOR FILING DATE: 2002-12-19
;    PRIOR APPLICATION NUMBER: 60/369,877
;    PRIOR FILING DATE: 2002-04-05
;    PRIOR APPLICATION NUMBER: 60/384,828
;    PRIOR FILING DATE: 2002-06-04
;    PRIOR APPLICATION NUMBER: 60/396,591
;    PRIOR FILING DATE: 2002-07-18
;    PRIOR APPLICATION NUMBER: 60/403,370
;    PRIOR FILING DATE: 2002-08-15
;    PRIOR APPLICATION NUMBER: 60/425,737
;    PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
;    LENGTH: 243
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: CM085C11 scFv
US-10-981-691-53

  Query Match             91.8%;  Score 538;  DB 18;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 3.5e-42;
  Matches 102;  Conservative   5;  Mismatches   4;  Indels   0;  Gaps   0;

Qy      1  QSVLTQPPSVSAAPGQKVTISCSGSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
           |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    133  QSVLTQPPSVSAAPGQKVTISCSGSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy     61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
           |||||||||||||||||||||||| :|||||||||||||||| :||||
Db    193  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243
```

```
RESULT 9
US-10-727-155-309
; Sequence 309, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;    APPLICANT: John S. Babcock
;    APPLICANT: Jaspal S. Kang
;    APPLICANT: Orit Foord
;    APPLICANT: Larry Green
;    APPLICANT: Xiao Feng
;    APPLICANT: Scott Klakamp
;    APPLICANT: Mary Haak-Frendscho
;    APPLICANT: Palaniswami Rathanaswami
;    APPLICANT: Craig Pigott
;    APPLICANT: Meina Liang
;    APPLICANT: Rozanne Lee
;    APPLICANT: Kathy Manchulencho
;    APPLICANT: Raffaella Faggioni
;    APPLICANT: Giorgio Senaldi
;    APPLICANT: Qiaojuan Jane Su
;    TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;    TITLE OF INVENTION: FACTOR AND USES THEREOF
;    FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
;    PRIOR APPLICATION NUMBER: 60/430729
;    PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 309
;    LENGTH: 110
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-727-155-309

  Query Match             91.6%;  Score 537;  DB 17;  Length 110;
  Best Local Similarity   94.5%;  Pred. No. 1.9e-42;
  Matches 104;  Conservative   1;  Mismatches   5;  Indels   0;  Gaps   0;

Qy      1  QSVLTQPPSVSAAPGQKVTISCSGSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db      1  QSVLTQPPSVSAAPGQKVTISCSGSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 60

Qy     61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
           ||||||||||||||||||||||||| :|||||||||||||||| :||||
Db     61  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110
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RESULT 10
US-10-727-155-311
; Sequence 311, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;    APPLICANT: John S. Babcock
;    APPLICANT: Jaspal S. Kang
;    APPLICANT: Orit Foord
;    APPLICANT: Larry Green
;    APPLICANT: Xiao Feng
;    APPLICANT: Scott Klakamp
;    APPLICANT: Mary Haak-Frendscho
;    APPLICANT: Palaniswami Rathanaswami
;    APPLICANT: Craig Pigott
;    APPLICANT: Meina Liang
;    APPLICANT: Rozanne Lee
;    APPLICANT: Kathy Manchulencho
;    APPLICANT: Raffaella Faggioni
;    APPLICANT: Giorgio Senaldi
;    APPLICANT: Qiaojuan Jane Su
;    TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;    TITLE OF INVENTION: FACTOR AND USES THEREOF
;    FILE REFERENCE: ABGENIX.073A
```

```
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SEQ ID NO 311
  LENGTH: 110
  TYPE: PRT
  SOFTWARE: FastSEQ for Windows Version 4.0
  ORGANISM: Homo sapiens
US-10-727-155-311

Qy  1  QSVLTQPPSVSAAPGQKYTISCSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
       |||||||||||||||| |||||||| |||||| |||||||||||| ||||| |||||||
Db  1  QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy  61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVL 110
       ||||||||||||||||||||||||||||||||||||| ||||||||||
Db  61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110
```

```
RESULT 11
US-09-880-748-1260
Sequence 1260, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
  APPLICANT: Ruben et al.
  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
  FILE REFERENCE: PF523
  CURRENT APPLICATION NUMBER: US/09/880,748
  CURRENT FILING DATE: 2001-06-15
  PRIOR APPLICATION NUMBER: 60/293,499
  PRIOR FILING DATE: 2001-05-25
  PRIOR APPLICATION NUMBER: 60/240,816
  PRIOR FILING DATE: 2000-10-17
  PRIOR APPLICATION NUMBER: 60/212,210
  PRIOR FILING DATE: 2000-06-15
  PRIOR APPLICATION NUMBER: 60/276,248
  PRIOR FILING DATE: 2001-03-16
  PRIOR APPLICATION NUMBER: 60/277,379
  PRIOR FILING DATE: 2001-03-16
  PRIOR APPLICATION NUMBER: 60/277,379
  PRIOR FILING DATE: 2001-03-21
  NUMBER OF SEQ ID NOS: 3239
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1260
  LENGTH: 258
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-880-748-1260

Query Match       91.6%;  Score 537;  DB 17;  Length 110;
Best Local Similarity  94.5%;  Pred. No. 1.9e-42;
Matches 104;  Conservative 1;  Mismatches 5;  Indels 0;  Gaps 0;

Qy  1  QSVLTQPPSVSAAPGQKYTISCSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
       |||||||||||||||| |||||||| |||||| |||||||||||| ||||| |||||||
Db  1  QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy  61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVL 110
       ||||||||||||||||||||||||||||||||||||| ||||||||||
Db  61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110
```

```
RESULT 12
US-10-293-418-1260
Sequence 1260, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
  APPLICANT: Ruben et al.
  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
  FILE REFERENCE: PF523P2
  CURRENT APPLICATION NUMBER: US/10/293,418
  CURRENT FILING DATE: 2002-11-27
  PRIOR APPLICATION NUMBER: 60/331,469
  PRIOR FILING DATE: 2001-11-16
  PRIOR APPLICATION NUMBER: 60/340,817
  PRIOR FILING DATE: 2001-12-19
  PRIOR APPLICATION NUMBER: 09/880,748
  PRIOR FILING DATE: 2001-06-15
  PRIOR APPLICATION NUMBER: 60/293,499
  PRIOR FILING DATE: 2000-06-16
  PRIOR APPLICATION NUMBER: 60/240,816
  PRIOR FILING DATE: 2000-10-17
  PRIOR APPLICATION NUMBER: 60/212,210
  PRIOR FILING DATE: 2000-06-15
  PRIOR APPLICATION NUMBER: 60/276,248
  PRIOR FILING DATE: 2001-03-16
  PRIOR APPLICATION NUMBER: 60/277,379
  PRIOR FILING DATE: 2001-03-21
  NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1260
  LENGTH: 258
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-293-418-1260

Query Match       91.1%;  Score 534;  DB 10;  Length 258;
Best Local Similarity  92.8%;  Pred. No. 8.9e-42;
Matches 103;  Conservative 1;  Mismatches 7;  Indels 0;  Gaps 0;

Qy  1  QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
       |||||||||||||||||||||||||||||| |||||||||||| ||||| |||||||
Db  148 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 207

Qy  61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
       ||||||||||||||||||||||||||| |||  |||||||| |||||||
Db  208 DRFSGSKSGTSATLGITGLQTGDEADYYCGAWDSSLSAVVFGGSGTKLTVLG 258
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```
RESULT 13
US-09-880-748-1246
Sequence 1246, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
  APPLICANT: Ruben et al.
  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
  FILE REFERENCE: PF523
  CURRENT APPLICATION NUMBER: US/09/880,748
  CURRENT FILING DATE: 2001-06-15
  PRIOR APPLICATION NUMBER: 60/293,499
  PRIOR FILING DATE: 2001-05-25
  PRIOR APPLICATION NUMBER: 60/240,816
  PRIOR FILING DATE: 2000-10-17
  PRIOR APPLICATION NUMBER: 60/212,210
  PRIOR FILING DATE: 2000-06-15
  PRIOR APPLICATION NUMBER: 60/276,248
  PRIOR FILING DATE: 2001-03-16
  PRIOR APPLICATION NUMBER: 60/277,379
  PRIOR FILING DATE: 2001-03-21
  NUMBER OF SEQ ID NOS: 3239
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1246
  LENGTH: 248
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-880-748-1246

Query Match       91.0%;  Score 533;  DB 10;  Length 248;
Best Local Similarity  93.7%;  Pred. No. 1.1e-41;
Matches 104;  Conservative 1;  Mismatches 6;  Indels 0;  Gaps 0;

Qy  1  QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   138 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNNVSWYQQLPGTAPKLLIYDNNKRPSGIP 197
Qy    61 DRFSGSKSGTSATLGITGLQGTGDEADYYCXTWDSSLSAAVVFGGGTKLTVLG 111
Db   198 DRFSGSKSGTSATLGITGLQTGDEADYHCGTWDSSLVAAVFGGGTKLTVLG 248
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RESULT 14
US-10-293-418-1246
; Sequence 1246, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1246
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1246

Query Match   91.0%; Score 533; DB 15; Length 248;
Best Local Similarity 93.7%; Pred. No. 1.1e-41;
Matches 104; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          ||||||||||||||||||||||||||||||| |||||||||||| |||||| |||||||
Db 138 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNNVSWYQQLPGTAPKLLIYDNNKRPSGIP 197

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAAVVFGGGTKLTVLG 111
          ||||||||||||||||||| |||||||| ||||||| |||||||||||||||
Db 198 DRFSGSKSGTSATLGITGLQTGDEADYHCGTWDSSLVAAVFGGGTKLTVLG 248
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RESULT 15
US-10-269-805-10
; Sequence 10, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-10
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```
Query Match     90.8%;  Score 532;  DB 14;  Length 112;
Best Local Similarity  92.9%;  Pred. No. 5.7e-42;
Matches 104;  Conservative  2;  Mismatches  4;  Indels  2;  Gaps  1;

Qy    1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          |||||||||||||||||||||||||||||||:|||||||||||||||:|:||.|||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA--VVFGGGTKLTVL 110

Qy   61 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 197
          ||||||||||||||||||||||||||||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAAEVVFGGGTKLTVL 112
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Search completed: October 13, 2005, 03:02:48
Job time : 111.575 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 13, 2005, 02:37:04 ; Search time 18.5923 Seconds
                                              (without alignments)
                                              457.717 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI..........SLSAVVPGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	544	92.8	234	4	US-09-372-425A-4	Sequence 4, Appli
2	518	88.4	112	3	US-09-315-574A-3	Sequence 18, Appl
3	518	88.4	112	4	US-09-490-070A-18	Sequence 18, Appl
4	518	88.4	112	4	US-09-490-153-18	Sequence 18, Appl
5	518	88.4	112	4	US-09-490-324-18	Sequence 18, Appl
6	515	87.9	110	1	US-09-069-911-2	Sequence 2, Appl
7	515	87.9	114	4	US-09-240-274-62	Sequence 62, Appl
8	513.5	87.6	112	3	US-08-983-607-31	Sequence 31, Appl
9	494.5	84.4	132	2	US-08-345-321-4	Sequence 4, Appl
10	493	84.1	109	3	US-09-240-274-61	Sequence 61, Appl
11	486	82.9	111	2	US-09-240-274-36	Sequence 36, Appl
12	486	82.9	111	2	US-09-315-574-36	Sequence 36, Appl
13	486	82.9	258	4	US-08-665-202-5	Sequence 5, Appli
14	486	82.9	258	4	US-09-315-574-5	Sequence 5, Appli
15	486	82.9	262	4	US-09-069-821-4	Sequence 4, Appli
16	486	82.9	262	4	US-09-956-086-4	Sequence 4, Appli
17	486	82.9	262	4	US-09-956-087-4	Sequence 4, Appli
18	486	82.9	282	3	US-09-420-592A-7	Sequence 7, Appli
19	486	82.9	282	4	US-09-983-580-7	Sequence 7, Appli
20	486	82.9	282	4	US-09-985-442-7	Sequence 7, Appli
21	485	82.8	111	2	US-08-665-202-42	Sequence 42, Appl
22	485	82.8	111	2	US-09-315-574-42	Sequence 42, Appl
23	484	82.6	98	2	US-08-665-202-37	Sequence 37, Appl
24	484	82.6	98	2	US-09-315-574-37	Sequence 37, Appl
25	484	82.6	111	2	US-08-665-202-43	Sequence 43, Appl
26	484	82.6	111	4	US-09-315-574-43	Sequence 43, Appl
27	482	82.3	111	3	US-08-983-607-35	Sequence 35, Appl
28	480	81.9	111	2	US-08-665-202-40	Sequence 40, Appl
29	480	81.9	111	4	US-09-315-574-40	Sequence 40, Appl
30	479.5	81.8	111	2	US-08-665-202-39	Sequence 39, Appl
31	479.5	81.8	112	4	US-09-315-574-39	Sequence 39, Appl
32	479	81.7	236	4	US-08-487-550-10	Sequence 10, Appl
33	479	81.7	236	4	US-09-526-098-10	Sequence 10, Appl
34	479	81.7	236	4	US-09-383-916-10	Sequence 10, Appl
35	474.5	81.0	236	4	US-09-049-672A-7	Sequence 7, Appli
36	466	79.5	113	1	US-08-211-202-113	Sequence 113, App
37	465	79.5	111	4	US-08-211-202-112	Sequence 112, App
38	463	79.0	109	4	US-09-424-840B-8	Sequence 8, Appli
39	454	77.5	109	1	US-09-240-274-54	Sequence 54, Appli
40	454	77.5	111	2	US-08-665-202-41	Sequence 41, Appl
41	454	77.5	111	4	US-09-315-574-41	Sequence 41, Appl
42	450	76.8	111	4	US-08-652-816A-15	Sequence 15, Appl
43	450	76.8	111	2	US-08-211-202-113	Sequence 113, App
44	448	76.5	109	3	US-09-025-769B-32	Sequence 32, Appl
45	448	76.5	109	3	US-09-025-769B-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-372-425A-4
; Sequence 4, Application US/09372425A
; Patent No. 6475749
; GENERAL INFORMATION:
; APPLICANT: Sherle L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
;   STREET: 2029 Century Park East, Suite 3800
;   CITY: Los Angeles
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 90067
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy Disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: Windows 98
;   SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/372,425A
; APPLICATION NUMBER:
;   FILING DATE: August 11, 1999
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Oldenakmp, David J.
;   REGISTRATION NUMBER: 29,421
;   REFERENCE/DOCKET NUMBER: 510015-223
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (310) 788-5000
;   TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 234 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Light chain - AA
US-09-372-425A-4

Query Match   92.8%; Score 544; DB 4; Length 234;
Best Local Similarity   90.4%; Pred. No. 4.1e-46;
Matches 103; Conservative   5; Mismatches   6; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||

Db   19 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNYVSWYQHFPGTAPKLLIYDNNQRPSGIP 78
Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
Db   79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVLFGGGTEVTVLGQPK 132

RESULT 2
US-09-025-769B-18
; Sequence 18, Application US/0902576B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-18

Query Match   88.4%;   Score 518; DB 3;   Length 112;
Best Local Similarity   87.5%;
Matches 98; Conservative   5; Mismatches   9; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          |||||||||||:||||||||||||||||||||||:||||||||||:|||||||||:|||||:|
Db   1 QSVLTQPPSVSGAPGQRVTISCSGSGSSSNIGNNVVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
          ||||||||||||:|||||::||:|||||||:||||||:|||||||||||||
Db   61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDSLSGVVFGGGTKLTVLGQ 112

RESULT 3
US-09-490-070A-18
; Sequence 18, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim

;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;   White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-070A-18

Query Match   88.4%;   Score 518; DB 4;   Length 112;
Best Local Similarity   87.5%;
Matches 98; Conservative   5; Mismatches   9; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          |||||||||||:||||||||||||||||||||||:||||||||||:|||||||||:|||||:|
Db   1 QSVLTQPPSVSGAPGQRVTISCSGSGSSSNIGNNVVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
          ||||||||||||:|||||::||:|||||||:||||||:|||||||||||||
Db   61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDSLSGVVFGGGTKLTVLGQ 112

RESULT 4
US-09-490-153-18
; Sequence 18, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;   Pack, Peter
;   Ilag, Vic
;   Ge, Liming
;   Moroney, Simon
;   Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York

RESULT 5
US-09-490-324-18
; Sequence 18, Application US/0940324
; Patent No. 6828422
; GENERAL INFORMATION:
    APPLICANT: Knappik, Achim
             Pack, Peter
             Ilag, Vic
             Ge, Liming
             Moroney, Simon
             Plueckthun, Andreas
    TITLE OF INVENTION: Protein/(Poly)peptide libraries
    NUMBER OF SEQUENCES: 373
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
        STREET: 1251 Avenue of the Americas
        CITY: New York
        STATE: New York
        COUNTRY: USA
        ZIP: 10021
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/490,324

    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US/09/025,769B
        FILING DATE: 18-FEB-1998
        APPLICATION NUMBER: US/09/490,153
        FILING DATE: 24-Jan-2000
        APPLICATION NUMBER: EP 95 11 3021.0
        FILING DATE: 18-AUG-1995
    ATTORNEY/AGENT INFORMATION:
        NAME: James F. Haley, Jr., Esq.
        REGISTRATION NUMBER: 27,794
        REFERENCE/DOCKET NUMBER: MORPHO/5
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (212)596-9000
        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 112 amino acids
        TYPE: amino acid
        STRANDEDNESS: <Unknown>
        TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match   88.4%; Score 518; DB 4; Length 112;
Best Local Similarity   87.5%; Pred. No. 6.4e-44;
Matches   98; Conservative   5; Mismatches   9; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
              ||||||||||||| ||| :|||||||||||||||||||||||||||||||||: ||:|
Db   1 QSVLTQPPSVSGAPGQRVTISCSGSGSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy   61 DRFSGSKSGTSASLAITGLQSEDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
              |||||||||||||:|: ||||||| ||| ||| |||||||||||||||||||
Db   61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDSLSGVVFGGGTKLTVLGQ 112

RESULT 6
US-08-199-911-2
; Sequence 2, Application US/08199911
; Patent No. 5495002
; GENERAL INFORMATION:
    APPLICANT: Kobrin, Barry J.
    APPLICANT: Haspel, Martin V.
    TITLE OF INVENTION: Tumor Associated Monoclonal Antibody
    TITLE OF INVENTION: 123AV16
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: AKZO NOBEL
        STREET: 1330 Piccard Drive
        CITY: Rockville
        STATE: Maryland
        COUNTRY: USA
        ZIP: 20850
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/199,911
        FILING DATE: 22-FEB-1994
        CLASSIFICATION: 435
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/065,517
        FILING DATE: 21-MAY-1993
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/636,179
        FILING DATE: 31-DEC-1994
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/302,155
        FILING DATE: 25-JAN-1989
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 06/697,078

STATE: New York
    COUNTRY: USA
    ZIP: 10021
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/490,153
    FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/025,769B
    FILING DATE: 18-FEB-1998
    APPLICATION NUMBER: US/09/490,153
    FILING DATE: 24-Jan-2000
    APPLICATION NUMBER: EP 95 11 3021.0
    FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
    NAME: James F. Haley, Jr., Esq.
    REGISTRATION NUMBER: 27,794
    REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (212)596-9000
    TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 112 amino acids
        TYPE: amino acid
        STRANDEDNESS: <Unknown>
        TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-153-18

Query Match   88.4%; Score 518; DB 4; Length 112;
Best Local Similarity   87.5%; Pred. No. 6.4e-44;
Matches   98; Conservative   5; Mismatches   9; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||| ||| :|||||||||||||||||||||||||||:||||||: ||:|
Db   1 QSVLTQPPSVSGAPGQRVTISCSGSGSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
              ||||||||||||:|: ||||| ||||| ||| ||| ||||||||||||||||
Db   61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDSLSGVVFGGGTKLTVLGQ 112

; FILING DATE: 31-JAN-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/575,533
; FILING DATE: 31-JAN-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-199-911-2

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Qy   Query Match     87.9%; Score 515; DB 1; Length 110;
     Best Local Similarity   89.1%; Pred. No. 1.2e-43;
Matches  98; Conservative  3; Mismatches  9; Indels  0; Gaps  0;

Qy  1 QSVLTQPPSVSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
        ||||||||||||||||||||||||||||||||||||||||||||| |:|
Db  1 QSALTQPPSVSVSAAPGQKVTISCSGSGTSSNIGNNFVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy 61 DRFSGSKSGTSATLGITGLQTGDEADYYCXXTWDSSLSAVFGGGGTKLTVL 110
        ||||||||||||||||||||||||||| ||||||| ||||||||||
Db 61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDTRLRAGVFGGGGTKLTVL 110
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RESULT 7
US-09-240-274-62
; Sequence 62, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LENGTH: 114
; OTHER INFORMATION: anti-Rh(D) chain NO2
US-09-240-274-62

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Qy   Query Match     87.9%; Score 515; DB 3; Length 114;
     Best Local Similarity   90.2%; Pred. No. 1.3e-43;
Matches 101; Conservative  2; Mismatches  5; Indels  4; Gaps  1;

Qy  4 LTQPPSVSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPDRF 63
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3 LTQPPSVSAAPGQKVTISCSGSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRF 62

Qy 64 SGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA----VVFGGGGTKLTVLG 111
        |||||||||||||||||||||||||           |||||||||||||
Db 63 SGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGRVRMFGGGGTKLTVLG 114
```

RESULT 8
US-08-983-607-31
; Sequence 31, Application US/08983607
; Patent No. 6140470

; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION:
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V73
; FEATURE:
; NAME/KEY: light chain
US-08-983-607-31

```
Qy   Query Match     87.6%; Score 513.5; DB 3; Length 112;
     Best Local Similarity   90.2%; Pred. No. 1.8e-43;
Matches 101; Conservative  3; Mismatches  7; Indels  1; Gaps  1;

Qy  1 QSVLTQPPSVSVSAAPGQKVT-ISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGI 59
        |||||||||||||||||||| |||||||||||||||||||||||| |||||||||
Db  1 QSALTQPPSVSVSAAPGQKVTXISCSGSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGI 60

Qy 60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGGTKLTVLG 111
        ||||||||||||||||||||||||||| |||||||| ||||:|||
Db 61 PDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEVFGTGTQLTVLG 112
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RESULT 9
US-08-345-321-4
; Sequence 4, Application US/08345321
; Patent No. 5914109
; GENERAL INFORMATION:
; APPLICANT: ZOLLA-PAZNER, Susan

APPLICANT: GORNY, Miroslav K.
TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HIV-1
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,675
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ZOLLA-PAZNER1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-345-321-4

RESULT 10
US-09-240-274-61
Sequence 61, Application US/0924O274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US/09/240,274
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens

Query Match   84.4%;   Score 494.5; DB 2; Length 132;
Best Local Similarity   88.3%; Pred. No. 1.6e-41;
Matches   98; Conservative   2; Mismatches 10; Indels   1; Gaps   1;

```
Qy  1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
      |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db 20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIPNNYVLWYQQFPGTAPKLLIFDNYRRPSGIP 79

Qy 61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA-VFGGGTKLTVL 110
      |||||||||||||||||||||||||||||  |   |||  |||||||||
Db 80 DRFSGSKSGTSATLGITGLQTGDEADYFCATWDSGLSADWVFGGGTKLTVL 130
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FEATURE:
OTHER INFORMATION: anti-Rh(D) chain NO1
US-09-240-274-61

Query Match   84.1%;   Score 493; DB 3; Length 109;
Best Local Similarity   87.9%; Pred. No. 1.8e-41;
Matches   94; Conservative   5; Mismatches   8; Indels   0; Gaps   0;

```
Qy  4 LTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPDRF 63
      |||||||||||||||||||||||||| :|| ||||||||||:|||: : :|||||||||||
Db  3 LTQPPSVSAAPGQKVTISCSGSSSNIDSNYVSWYQQLPGTAPKLLIFDNYRRPSGIPDRF 62

Qy 64 SGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
      ||||||||||||||||||||||||| |||| :|  ||||||||||
Db 63 SGSKSGTSATLGITGLQTGDEADYYCATWDDSLNGRVFGGGTKLTVL 109
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RESULT 11
US-08-665-202-36
Sequence 36, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307B-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acid
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-36

Query Match   82.9%;   Score 486; DB 2; Length 111;
Best Local Similarity   82.9%; Pred. No. 9.1e-41;
Matches   92; Conservative   7; Mismatches 12; Indels   0; Gaps   0;

```
Qy  1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
      ||||||||||||||||||||||||||||||| ||||||||||:|||| : :|||:|| :|
Db  1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNVSWYQQLPGTAPKLLIYGHTNRPAGVP 60
```

RESULT 12
US-09-315-574-36
; Sequence 36, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
;   APPLICANT: Marks, James D.
;   APPLICANT: Schier, Robert
;   TITLE OF INVENTION: Tumor Antigens
;   TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
;   NUMBER OF SEQUENCES: 141
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
;   STREET: Four Embarcadero Center, Suite 1100
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-4106
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/315,574
;   FILING DATE: 20-MAY-99
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/000,238
;   FILING DATE: 14-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/000,250
;   FILING DATE: 15-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/665,202
;   FILING DATE: 13-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Hunter, Tom
;   REGISTRATION NUMBER: 38,498
;   REFERENCE/DOCKET NUMBER: 02307E-061411
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 36:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 111 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide

US-09-315-574-36

Query Match   82.9%;   Score 486;   DB 4;   Length 111;
Best Local Similarity 82.9%; Pred. No. 9.1e-41;
Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
      |||||||||||||||||||||||||||||||||||||||:|||||||||:|:|
Db   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGHTNRPAGVP 60

Qy 61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
      ||||||||||||||||||||||||||:|:||||||||||||||||||
Db 61 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 111

RESULT 13
US-08-665-202-5
; Sequence 5, Application US/08665202
; Patent No. 5977322

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-315-574-5

Query Match 82.9%; Score 486; DB 4; Length 258;
Best Local Similarity 82.9%; Pred. No. 2.4e-40;
Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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Qy    1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP  60
        ||||||||||||||||||||||||||||||||| ||||||||||:| |||| |:|:|
Db  145 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNVVSWYQQLPGTAPKLLIYGHTNRPAGVP 204

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
        ||||||||||||| || |: :: |||||| |: :: :|||||||||||||
Db  205 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 255
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FILING DATE: 30-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-09-069-821-4

Query Match 82.9%; Score 486; DB 3; Length 262;
Best Local Similarity 82.9%; Pred. No. 2.5e-40;
Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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Qy    1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP  60
        ||||||||||||||||||||||||||||||||| ||||||||||:| |||| |:|:|
Db    1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNVVSWYQQLPGTAPKLLIYGHTNRPAGVP  60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
        ||||||||||||| || |: :: |||||| |: :: :|||||||||||||
Db   61 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 111
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Search completed: October 13, 2005, 02:45:19
Job time : 18.5923 secs

RESULT 15
US-09-069-821-4
Sequence 4, Application US/09069821
Patent No. 6323322
GENERAL INFORMATION:
APPLICANT: FILPULA, DAVID
APPLICANT: WANG, MAOLIANG
APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LIHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821

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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 13, 2005, 02:45:26 ; Search time 113.511 Seconds
(without alignments)
514.286 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKYTI..........SLSAVVFGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description	
1	524	111	1	P01702	LV1D_HUMAN	homo sapien
2	523	130	1	P01701	LV1G_HUMAN	homo sapien
3	515	110	2	Q8TE63	Q8TE63	homo sapien
4	508	111	1	P01701	LV1C_HUMAN	homo sapien
5	507	235	2	Q6IN99	Q6IN99	homo sapien
6	481	101	2	Q8IZD8	Q8IZD8	homo sapien
7	472.5	236	2	Q6GMX4	Q6GMX4	homo sapien
8	468	109	1	P01703	LV1I_HUMAN	homo sapien
9	463	235	2	Q6GMW6	Q6GMW6	homo sapien
10	461.5	236	2	Q8NEJ1	Q8NEJ1	homo sapien
11	436.5	112	1	P01700	LV1B_HUMAN	homo sapien
12	436.5	236	2	Q6GMX3	Q6GMX3	homo sapien
13	430.5	236	2	Q96E61	Q96E61	homo sapien
14	430.5	236	2	Q6GMV7	Q6GMV7	homo sapien
15	421	237	2	Q6DHW4	Q6DHW4	homo sapien
16	420.5	236	2	Q6IPQ0	Q6IPQ0	homo sapien
17	417.5	233	2	Q6PJA3	Q6PJA3	homo sapien
18	417	109	1	P01708	LV1F_HUMAN	homo sapien
19	415.5	112	1	P06887	LV1H_HUMAN	homo sapien
20	415	111	1	P01699	LV1A_HUMAN	homo sapien
21	413.5	236	2	Q6PIQ7	Q6PIQ7	homo sapien
22	403	235	2	Q6PIK1	Q6PIK1	homo sapien
23	400	108	2	Q96SB0	Q96SB0	homo sapien
24	394.5	236	2	Q6PS53	Q6PS53	homo sapien
25	386	116	2	Q96SD0	Q96SD0	homo sapien
26	385.5	234	2	Q8N355	Q8N355	homo sapien
27	385	111	1	P01712	LV2I_HUMAN	homo sapien
28	383.5	112	1	P04209	LV2K_HUMAN	homo sapien
29	382	111	1	P01707	LV2D_HUMAN	homo sapien
30	378.5	234	2	Q6GMW3	Q6GMW3	homo sapien
31	378	235	2	Q6PJG0	Q6PJG0	homo sapien
32	371	111	1	P80748	LV3B_HUMAN	homo sapien
33	369	111	1	P01706	LV2C_HUMAN	homo sapien
34	369	111	1	P01710	LV2G_HUMAN	homo sapien
35	368	111	1	P01709	LV2F_HUMAN	homo sapien
36	366	111	1	P01711	LV1E_HUMAN	homo sapien
37	364	103	1	P01703	LV2H_HUMAN	homo sapien
38	363	109	1	P01711	LV2B_HUMAN	homo sapien
39	363	235	2	Q6P2Z1	Q6P2Z1	homo sapien
40	362	235	2	Q6NS96	Q6NS96	homo sapien
41	360	111	1	P01715	LV4A_HUMAN	homo sapien
42	359	106	1	P06889	LV4E_HUMAN	homo sapien
43	359	111	1	P01705	LV2B_HUMAN	homo sapien
44	356	233	2	Q8TBC9	Q8TBC9	homo sapien
45	353	233	2	Q8N5F4	Q8N5F4	homo sapien

ALIGNMENTS

RESULT 1
LV1D_HUMAN
ID LV1D_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subsubgroup.";
RL J. Biochem. 93:421-429(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01965; L1HUNG.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 105 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 89 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 89.4%; Score 524; DB 1; Length 111;
Best Local Similarity 90.1%;
Matches 100; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Qy     1  QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP  60
          ||||||||||||||||||||||||||||||:||||||||||||||:|||||| ||::||||
Db     1  QSVLTQPPSVSAAPGQEVTISCSGSSSNIGDNFVSWYQQLPGTAPKLLIYDNNKRPSGIP  60

Qy    61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG         111
          ||||||||||||||||||||| |||||||  ||||||:|||||||||||||
Db    61  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSVGMFGGGTRVTVLG         111
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RESULT 2
LV1G_HUMAN

```
ID   LV1G_HUMAN     STANDARD;      PRT;   130 AA.
AC   P06316;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region BL2 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85062823; PubMed=6095199;
RA   Tsujimoto Y., Croce C.M.;
RT   "Molecular cloning of a human immunoglobulin lambda chain variable
RT   sequence.";
RL   Nucleic Acids Res. 12:8407-8414(1984).
```

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DR   EMBL; X01147; CAA25598.1; -.
DR   PIR; A01966; L1HUBL.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL      1     19
FT   CHAIN      20    130    Ig lambda chain V-I region BL2.
FT   DOMAIN     20    115    V segment.
FT   DOMAIN    116    130    J segment.
FT   DISULFID   41    108    By similarity.
FT   NON_TER   130    130
SQ   SEQUENCE   130 AA;  13564 MW;  FA44BB17D3A55EBF CRC64;

Query Match             89.2%;  Score 523;  DB 1;  Length 130;
Best Local Similarity   90.1%;  Conservative   5;  Pred. No. 2e-43;  Mismatches   6;  Indels   0;  Gaps   0;
Matches  100;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              QSVLTQPPSVSAAPGQKVTISCSGSSSSNIGNN FVSWYQQLPGTAPXLLIYDITKRPSGIP
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSSNIGNDVSVSWYQQVPGTAPKLLIYDNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTKLTVLG
Db         80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTKLTVLG 130
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RESULT 3
ID   Q8TE63         PRELIMINARY;    PRT;   110 AA.
AC   Q8TE63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin light chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95007525; PubMed=7923137;
RA   Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
RT   "Establishment, molecular rescue, and expression of 123AV16-1, a
RT   tumor-reactive human monoclonal antibody.";
RL   Cancer Res. 54:5178-5185(1994).
DR   EMBL; L33985; AAL68704.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     1      1
FT   CHAIN      <1   >110    Immunoglobulin light chain variable
FT                           region.
FT   NON_TER   110    110
SQ   SEQUENCE   110 AA;  11479 MW;  599D1628F8F54437C CRC64;

Query Match             87.9%;  Score 515;  DB 2;  Length 110;
Best Local Similarity   89.1%;  Conservative   3;  Pred. No. 1e-42;  Mismatches   9;  Indels   0;  Gaps   0;
Matches   98;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              QS LTQPPSVSAAPGQKVTISCSGSSSSNIGNNFVSWYQQ PGTAPKLLIYDNNKRPSGVP
Db          1 QSALTQPPSVSAAPGQKVTISCSGSSSSNIGNNFVSWYQQFPGTAPKLLIYDNNKRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDTRLRAGVFGGGTKLTVL
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDTRLRAGVFGGGTKLTVL 110
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```
RESULT 4
ID   LVIC_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01701;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-I region NEW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69008092; PubMed=4177823;
RA   Langer B., Steinmetz-Kayne M., Hilschmann N.;
RT   "The complete amino acid sequence of Bence Jones protein New (lambda-
RT   type). Subgroups in the variable part of immunoglobulin L-chains of
RT   the lambda-type.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01964; L1HUNW.
DR   HSSP; P01703; 7FAB.
GO   GO; GO:0005576; C:extracellular; NAS.
GO   GO; GO:0003823; F:antigen binding; NAS.
GO   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   DOMAIN      1    105    Ig-like.
FT   MOD_RES     1      1    Pyrrolidone carboxylic acid.
FT   DISULFID   22     89    By similarity.
FT   NON_TER   111    111
SQ   SEQUENCE   111 AA;  11453 MW;  AAECBCA3C49F2AD3 CRC64;

Query Match             86.7%;  Score 508;  DB 1;  Length 111;
Best Local Similarity   86.5%;  Conservative   7;  Pred. No. 5e-42;  Mismatches   8;  Indels   0;  Gaps   0;
Matches   96;
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RESULT 5

ID	Q6IN99;
AC	Q6IN99;
	PRELIMINARY; PRT; 235 AA.
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	IGLC2 protein.
GN	Name=IGLC2;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Pancreas;
RX	MEDLINE=22238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
	[2]

Qy	1	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP	60
		|||||||||:|||||||||||||||||||||||||||:|||||||||||||	
Db	1	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYEDNKRPSGIP	60

Qy	61	DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG	111
		|||||||||||||:|||||||:||||||||||||||||||||||	
Db	61	DRISASKSGTSATLGITGLRTGDEADYYCATWDSSLSNAVVFGGGTKVTVLG	111

RESULT 6

ID	Q8IZD8;
AC	Q8IZD8;
	PRELIMINARY; PRT; 101 AA.
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Anti-thyroglobulin light chain variable region (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Jang Y.-J., Chung J., Park J.-Y.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AY145444; AAN64328.1; -.
DR	HSSP; P01703; 7FAB.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_V.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
FT	NON_TER 1 1
FT	NON_TER 101 101
SQ	SEQUENCE 101 AA; 1506C2D9ACBA793 CRC64;

Qy	11	SAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPDRFSGSKSGT	70
		|||||||||||||||||||||||||||||||||:|||||:||:|	
Db	1	SAAPGQKVTISCSGSSSNIGKNVVSWYQQVPGTAPQLILIHDTDKRPSGIPDRFSGSQSGT	60

Qy	71	SATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG	111
		|||||||||||||:||||||||||||:|||	
Db	61	SATLGITGLRTGDEADYYCGTWTDSLSLAAVVFGGGTKLTVLG	101

RESULT 7

ID	Q6GMX4;
AC	Q6GMX4;
	PRELIMINARY; PRT; 236 AA.
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Spleen;
RX	MEDLINE=22238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RESULT 6 (continued)

Db	20	QSVLTQPPSVSAAPGQRVTISCSGSGSSNIGSNTVSWYQQPPGAAPQLLIYDNDKRPSGIP	79

Qy	61	DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK	114
		|||||||||||||||||:||||||:||||||||||||||||||:||	
Db	80	DRFSGSKSGTSATLAITGLQTEDEAEYYCGTWDTSLTAGVFGGGTKLTVLSQPK	133

Query Match   86.5%; Score 507; DB 2; Length 235;
Best Local Similarity   85.1%; Pred. No. 1.5e-41;
Matches 97; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy	1	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP	60
		|||||||||||||||||||||||||||||||||||||||||||||	

Query Match   82.1%; Score 481; DB 2; Length 101;
Best Local Similarity   90.1%; Pred. No. 2e-39;
Matches 91; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

SQ | SEQUENCE   235 AA;   24888 MW;   90C95D5E87A6BCC1 CRC64;
SQ | SEQUENCE   236 AA;   10374 MW;   1506C2D9ACBA793 CRC64;

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUB=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073769; AAH73769.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24809 MW; BA0AF0F419236A A5 CRC64;

Query Match   80.6%; Score 472.5; DB 2; Length 236;
Best Local Similarity   80.0%; Pred. No. 3.5e-38;
Matches 92; Conservative   9; Mismatches 13; Indels 1; Gaps 1;

```
Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSSNIGNNP-VSWYQQLPGTAPXLLIYDITKRPSGI 59
         |||||||||||||||::|||||||||||||||||| :|:||||||||||||||||:|||||
Db  20 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNSNRPSGV 79

Qy  60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXIWDSSLSAVVFGGGTKLTVLGQPK 114
         ||||||||||||||||||||||||||||||| |||:||||||||||||||||||||
Db  80 PDRFSGSKSGTSASLAITGLQARDEADYYCCQSYDSSLSGVMFGGGTKLTVLGQPK 134
```

RESULT 8
ID LV1I_HUMAN   STANDARD;   PRT;   109 AA.
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86000126; PubMed=3929803;
RA Toft K.G., Sletten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
RT containing amyloid fibril protein EPS (immunoglobulin light chain,
RT type lambda).";
RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC -!- MISCELLANEOUS: Residues 1-2, 56-62, and 74-78 and the sequenced
CC   peptides were positioned by homology.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A24456; L1HUEP.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin V region.
FT DOMAIN   1   105
FT CARBOHYD   104   104   N-linked (GlcNAc...).
FT DISULFID   22   89   By similarity.
FT NON_TER   109   109
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5AC73 CRC64;

Query Match   79.9%; Score 468; DB 1; Length 109;
Best Local Similarity   81.1%; Pred. No. 4.1e-38;
Matches 90; Conservative   9; Mismatches 10; Indels 2; Gaps 1;

```
Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
         |||||||||||||||||||:||:||||||||||| |:|:||||||||||||||||:||||||
Db   1 QSVLTQPPSLSAAPGQRVSICSGSSSSNIGKNYVDWYQQLPGTAPKLLIFNNNKRPSGIP 60

Qy  61 DRFSGSKSGTSATLGITGLQTGDEADYYCXIWDSSLSAVVFGGGTKLTVLG 111
         |||||||||||||||||||||||||||| |||:||||||||||||:||:|||
Db  61 DRFSGSKSGTSATLGITGLQTGDEAIYYCGTWDNRRS--VFGGGTNVTVVG 109
```

RESULT 9
ID Q6GMW6   Q6GMW6   PRELIMINARY; PRT;   235 AA.
AC Q6GMW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUB=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUB=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073784; AAH73784.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.

DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA; 24803 MW; 058B05F61118F1B8 CRC64;

Qy   Query Match
     Best Local Similarity   79.0%;   Score 463; DB 2; Length 235;
     Matches 87; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
        ||||||||| |:||| | |||||||||||||||||||||||| | ||| |:|||| :|:||
Db   20 QSVLTQPPSASGTPGQRRVTISCSGSSSNIGSNSVNWYQQFPGTAPKLLIYGNHQRPSGVP 79

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
        |||||||||||||:||| ||| :|:|||| | || |:||||||| |||||||
Db   80 DRFSGSKSGTSASLAISGLQSEDEADYYCGTWDDSLTGVFGVGTKVTVLGQPK 133

RESULT 10
ID   Q8NEJ1
AC   Q8NEJ1;
     PRELIMINARY;   PRT;   236 AA.
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Griwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SQ   SEQUENCE   236 AA; 25024 MW; 1703B77942630E08 CRC64;

Qy   Query Match   78.8%;   Score 461.5; DB 2; Length 236;
     Best Local Similarity   76.5%;   Pred. No. 4.2e-37;
     Matches 88; Conservative 11; Mismatches 15; Indels 1; Gaps 1;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGI 60
        ||||||||| | || | ||||||||||||||||||||| ||| | ||| ||:|| :|||
Db   20 QSVLTQPPSASGSPGQRVTISCSGSGSSSNIGSNYVYWYQQVPGTAPKLLIYRNDQRPSGV 79

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA-VVFGGGTKLTVLGQPK 114
        ||||||||||||:|| ||| :|:|||| | |||| :| ||||||| |||| |
Db   80 DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDSLSVHVVFGGGTQLTVL 134

RESULT 11
ID   LV1B_HUMAN
AC   P01700;
     STANDARD;   PRT;   112 AA.
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-I region HA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71038024; PubMed=5532227;
RA   Shinoda T., Titani K., Putnam F.W.;
RT   "Amino acid sequence of human lambda chains. II. Chymotryptic peptides
RT   and sequence of protein Ha.";
RL   J. Biol. Chem. 245:4475-4487(1970).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01963; L1HUHA.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN   1   106   Ig-like.
FT   MOD_RES   1   1   Pyrrolidone carboxylic acid.
FT   DISULFID   22   90   By similarity.
FT   NON_TER   112   112
SQ   SEQUENCE   112 AA; 11896 MW; 8D73378F3F5CD039 CRC64;

Qy   Query Match   74.5%;   Score 436.5; DB 1; Length 112;
     Best Local Similarity   76.6%;   Pred. No. 5.1e-35;
     Matches 85; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSN-IGNNFVSWYQQLPGTAPXLLIYDITKRPSGI 59
        ||||||||| | || | ||||||||||||| ||||:| |:| |:| | ||| ||:|| :||
Db   1 QSVLTQPPSVSGTPGQRVTISCSGSGSSSNGTGNNYVVSWYQQLPGTAPKLLIYRDDKRPSGV 60

Qy   60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
        |||||||||||||:|| ||| :|:|||| | |||| :|||||||| |||
Db   61 PDRFSGSKSGTSASLAISGLRSEDEAHYHCAAWDYRLSAVVFGGGTQLTVL 111

RESULT 12
ID   Q6GMX3
AC   Q6GMX3;
     PRELIMINARY;   PRT;   236 AA.
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073770; AAH73770.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   InterPro; PF00047; Ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA; 24700 MW; BC0B94DF4F2DCB7 CRC64;

RESULT 13

ID   Q96B61
AC   Q96B61
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).

Query Match   74.5%; Score 436.5; DB 2; Length 236;
Best Local Similarity   74.8%; Pred. No. 1.2e-34;
Matches 86; Conservative 10; Mismatches 18; Indels 1; Gaps 1;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNF-VSWYQQLPGTAPXLLIYDTIKRPSGI 59
           |||||||||||||||||||||||||||||| |||||||||||| ||||||: |||||
Db   20 QSVLTQPPSVSGAPGQVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLISNSNRPSGV 79

Qy   60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAAVFGGGTKLTVLGQPK 114
           |||||||||||||||||| ||| |||||||||||||||| ||||||||||||
Db   80 PDRFSGSKSGTSASLAIAGLQAEDEADYYCQSYDDSLTGRVFGGGTRLTVLSQPK 134

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   PIR; S12440; S12440.
DR   HSSP; P01842; 1AQK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

RESULT 14

ID   Q6GMV7
AC   Q6GMV7
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.

Query Match   73.5%; Score 430.5; DB 2; Length 236;
Best Local Similarity   73.0%; Pred. No. 4.5e-34;
Matches 84; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNF-VSWYQQLPGTAPXLLIYDTIKRPSGI 59
           |||||||||||| ||||||||||||||||| |||||||||||| ||||: |||||
Db   20 QSVLAQPPSVSGAPGQVTISCTGSSSNIGAGYAVHWYQQPPGAAPKVLIYGNYNRPSGV 79

Qy   60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAAVFGGGTKLTVLGQPK 114
           ||||||||||||||||| ||| ||||||||||||||||| ||||||||||||
Db   80 PDRFSGSKSGTSASLAIAGLQAEDEADYYCQSYDGSLSGSVFGAGTKVTVLSQPK 134

RESULT 15
Q6DHW4
ID   Q6DHW4   PRELIMINARY;   PRT;   237 AA.
AC   Q6DHW4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC075843; AAH75843.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein; UNKNOWN_1.
SQ   SEQUENCE 237 AA; 25108 MW; 68141170F7E784825 CRC64;

Query Match   71.8%; Score 422; DB 2; Length 237;
Best Local Similarity 70.7%; Pred. No. 3.9e-33;
Matches   82; Conservative   11; Mismatches   21; Indels   2; Gaps   1;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          ||||||| ||| ||||:|||||||| ||||| | ||||||||| |||: : :||| |
Db   20 QSVLTQPSSVSGTPGQRVTISCSGSSSNIGANNNVWYQQLPGTAPKLLIHTTNQRPSGVP 79

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLS--AVVFGGGGTKLTVLGQPK 114
          ||| ||||||:||| | || | ||| :|||||||:|:   :|||| ||||||| |||
Db   80 DRFGGSKSGTSASLAIGGLRSEDEAHYYCAAWDDSMSGPGYAFGTGTKVTVLRQPK 135

SEQUENCE FROM N.A.
TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073795; AAH73795.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein; UNKNOWN_1.
SQ   SEQUENCE 236 AA; 24950 MW; 3B04772474784TE930 CRC64;

Query Match   73.5%; Score 430.5; DB 2; Length 236;
Best Local Similarity 73.0%; Pred. No. 4.5e-34;
Matches   84; Conservative   11; Mismatches   19; Indels   1; Gaps   1;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          ||||||| ||| ||||:|||||||| ||||| | ||||||||| |||: :|||| |
Db   20 QSVLTQPSSVSGTPGQRVTISCSGSSSNIGANNNVWYQQLPGTAPKLLIHTTNQRPSGVP 79

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA-VVFGGGGTKLTVLGQPK 114
          |||||||||:||| | || | ||| :|||||||:|||| :||| ||||||||||||
Db   80 ERFSGSKSGPSASLVISGLQSEDEAEYYCAAWDDSLDGPYVFGTGTKVTVLGQPK 134

Search completed: October 13, 2005, 03:10:53
Job time : 114.511 secs

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OM protein - protein search, using sw model

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                GenCore version 5.1.6
                Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: October 13, 2005, 02:57:16 ; Search time 23.485 Seconds
(without alignments)
467.052 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI.........SLSAVVFGGGTKLTVLGQPK 114
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560	95.6	235	2	S05270	Ig lambda chain pr
2	539	92.0	111	2	S47009	Ig lambda chain V1
3	538	91.8	130	2	L1HUHA	Ig lambda chain V-
4	534	91.1	113	2	S09712	Ig lambda chain V
5	533	91.0	232	2	A29700	Ig lambda chain V
6	526	89.8	232	2	S25742	Ig lambda chain V
7	524	89.4	131	2	S24321	Ig lambda chain pr
8	523	89.2	111	2	L1HUNG	Ig lambda chain V-
9	523	89.2	130	1	L1HUBL	Ig lambda chain pr
10	520	88.7	111	1	S19664	Ig lambda chain pr
11	508	86.7	111	1	L1HUNW	Ig lambda chain V-
12	486	82.9	111	2	S47185	Ig lambda chain -
13	485	82.8	98	2	S36050	Ig lambda chain -
14	485	82.8	233	2	S25752	Ig lambda chain -
15	477	81.4	130	2	S78057	Ig lambda chain pr
16	474	80.9	216	2	A42193	Ig lambda chain (B
17	468	79.9	109	1	L1HUEP	Ig lambda chain V-
18	467	79.7	234	2	S25757	Ig lambda chain -
19	462	78.8	129	2	S78058	Ig lambda chain pr
20	462	78.8	233	2	S25744	Ig lambda chain -
21	461.5	78.8	235	2	S25750	Ig lambda chain -
22	459	78.3	149	2	S23626	Ig lambda chain V
23	457.5	78.1	216	2	S29258	Ig lambda chain V
24	452	77.1	213	2	S21066	Ig lambda chain V
25	452	77.1	112	2	B44151	Ig lambda chain V
26	451	77.0	112	2	C44151	Ig lambda chain V
27	447.5	76.4	112	2	PH0134	Ig lambda chain pr
28	447.5	76.4	140	2	S25746	Ig lambda chain -
29	447	76.3	236	2	D44151	Ig lambda chain V (K
30	442.5	75.6	235	2	S25754	Ig lambda chain -
31	440	75.1	110	1	S57408	Ig lambda chain v-
32	436.5	74.5	112	1	L1HUHA	Ig lambda chain v-
33	436	74.4	112	1	A44151	Ig lambda chain -
34	435.5	74.3	112	2	S51148	Ig antibody light cha
35	434.5	74.1	217	2	S55428	Ig light chain V-J
36	432	73.7	110	2	JB0246	Ig lambda chain NI
37	429	73.2	110	2	S57428	Ig light chain V-J
38	420	71.7	111	1	S36274	Ig lambda chain -
39	419	71.5	98	2	S25743	Ig lambda chain pr
40	419	71.5	117	2	S04525	Ig lambda chain -
41	417	71.2	109	1	L1HUWA	Ig lambda chain v-
42	415.5	70.9	112	1	L1HUNM	Ig lambda chain v-
43	415.5	70.9	140	2	PH0132	Ig lambda chain pr
44	415	70.8	111	1	L1HUVO	Ig lambda chain v-
45	409	69.8	111	2	S36263	Ig lambda chain v (K
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ALIGNMENTS

RESULT 1
S05270
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S05270; S04601
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05270
A;Molecule type: mRNA
A;Residues: 1-235 <KIS1>
A;Cross-references: EMBL:X14583; NID:g933394; PIDN:CAA32725.1; PID:g933395
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04601
A;Molecule type: mRNA
A;Residues: 1-130 <KIS2>
A;Cross-references: EMBL:X14583
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-235/Product: Ig lambda chain #status predicted <MAT>
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match    95.6%;  Score 560;  DB 2;  Length 235;
Best Local Similarity    94.7%;  Pred. No. 8.9e-41;
Matches 108;  Conservative 1;  Mismatches 5;  Indels 0;  Gaps 0;

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Qy    1  QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP  60
          QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNN:VSWYQQLPGTAPKLLIYD: KRPSGIP
Db   20  QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP  79

Qy   61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK  114
          DRFSGSKSGTSATLGITGLQTGDEADYYC TWDSS LS:A:VFGGGTKLTVLGQPK
Db   80  DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSRAGVFGGGTKLTVLGQPK  133
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RESULT 2
S47009
Ig lambda chain V1-J3 region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47009
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A;Reference number: S47009
A;Accession: S47009
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-111 <MAH>
A;Cross-references: EMBL:Z35495; NID:g517346; PIDN:CAA84629.1; PID:g517347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>

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Query Match          92.0%;  Score 539;  DB 2;  Length 111;
Best Local Similarity 93.7%;  Pred. No. 2.6e-39;
Matches 104; Conservative  2; Mismatches  5; Indels  0; Gaps  0;

Qy      1 QSVLTQPPSVSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          ||||||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||||
Db      1 QSVLTQPPSVSVSAAPGQKVTISCSGSGSSNIGNNYVSWYQQLPGTAPKLLIYENNKRPSGIP 60

Qy     61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
          ||||||||||||||||||||||||| ||||||||| |||||||||||||||
Db     61 DRFSGSKSGTSATLGITGLQTGDBADYYCGTWDSSLSAGVFGGGTKLTVLG 111
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RESULT 3
S09712
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09712
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains o
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <HUG>
A;Cross-references: GB:X52109; NID:g31454; PIDN:CAA36343.1; PID:g931455
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

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Query Match          93.6%;  Score 538;  DB 2;  Length 130;
Best Local Similarity 93.6%;  Pred. No. 3.8e-39;
Matches 103; Conservative  3; Mismatches  4; Indels  0; Gaps  0;

Qy      1 QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          ||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||||
Db      1 QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy     61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
          |||||||||||||||||| |||||||| ||||||||||||||||||||||
Db     80 DRFSGSKSGTSATLGITGLRTGDBADYYCATWDSSLSAVVFGGGTKLTVL 129
```

RESULT 4
A29700
Ig lambda chain V region (Zim) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C;Accession: A29700
A;Molecule type: protein
A;Residues: 1-113 <EUL>
R;Eulitz, M.; Breuer, M.; Linke, R.P.
Biol. Chem. Hoppe-Seyler 368, 863-870, 1987
A;Title: Is the formation of AL-type amyloid promoted by structural peculiarities of imm
A;Reference number: A29700; MUID:87299022; PMID:3620114
A;Accession: A29700
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>

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Query Match          91.1%;  Score 534;  DB 2;  Length 113;
Best Local Similarity 90.3%;  Pred. No. 7.2e-39;
Matches 102; Conservative  3; Mismatches  8; Indels  0; Gaps  0;
```

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Qy      2 SVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPD 61
          |||||||||||||||||||||||||| ||||||||||||||||| |||||| |||||||||
Db      1 SLLTQPPSVSAAPGQKVTISCSGSGSSNIANNYVSWYQQLPGTAPRLLIYENDKRPSGIPD 60

Qy     62 RFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
          ||||||| ||| ||||||||||||| ||||||||| ||||||||||||||||
Db     61 RFSGSKSDASVTLGITGLQTGDBADYYCGTWDSSLSAGVFGGGTKLTVLGQPK 113
```

RESULT 5
S25742
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25742
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25742
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COM>
A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

```
Query Match          91.0%;  Score 533;  DB 2;  Length 232;
Best Local Similarity 89.5%;  Pred. No. 1.8e-38;
Matches 102; Conservative  4; Mismatches  8; Indels  0; Gaps  0;

Qy      1 QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          |||||||||||||||||||||||||| ||||||||||||||||| |||||| ||||| |||
Db     17 QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNYVSWYQQLPGTAPRLLIFENNKRPSAIP 76

Qy     61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
          ||||||||||||||||||||||||| |||||||| |||||||||||||||||||
Db     77 DRFSGSKSGTSATLGITGLQTGDBADYYCGTWDSSLSLTDVVFGGGTKLTVLGQPK 130
```

RESULT 6
S24321
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24321
R;Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne,
Biochem. J. 285, 149-152, 1992
A;Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr
A;Reference number: S24319; MUID:92344562; PMID:1379039
A;Accession: S24321
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-131 <AUC>
A;Cross-references: EMBL:X64134; NID:g932808; PIDN:CAA45495.1; PID:g932809
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

```
Query Match          89.8%;  Score 526;  DB 2;  Length 131;
Best Local Similarity 90.2%;  Pred. No. 4e-38;
Matches 101; Conservative  3; Mismatches  8; Indels  0; Gaps  0;

Qy      1 QSVLTQPPSVSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          ||||||||||||||||||||||||||| ||||||||||||||||| |||||| |||||||||
Db     20 QSVLTQPPSVSAAPGQKVTISCSGSGSSNIANNYVSWYQQLPGTAPRLLIYENVRPSGIP 79

Qy     61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
          ||| ||||||||||||||||||||| ||||||||| ||| |||||||||||
Db     80 DRRSGSKSGTSATLGITGLQTGDBAEYYCGTWDSSLSGVEFGGGTKLTVLGQ 131
```

RESULT 7
L1HUNG
Ig lambda chain V-I region (Nig-64) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
A;Accession: A01965
A;Molecule type: protein
A;Residues: 1-111 <KAM>
C;Accession: A01965
R;Kametani, F.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
R;Tsujimoto, Y.; Croce, C.M.
A;Gene: GDB:IGLV@
A;Genetics:
A;Cross-references: GDB:119342; OMIM:147240
A;Title: Comparative studies on the structure of the light chains of human immunoglobuli
A;Reference number: A91970; MUID:83186114; PMID:6404900
C;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;15-91/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-89/Disulfide bonds: #status predicted

Query Match   89.4%; Score 524; DB 1; Length 111;
Best Local Similarity   90.1%; Pred. No. 5e-38;
Matches 100; Conservative   5; Mismatches   6; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSVSPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 60
          |||||||||||| ||||||||||||||||||||:|||||||||||||||:||||||||||||
Db   1 QSVLTQPPSVSAAPGQEVTISCSGSGSSSNIGNDVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
          ||||||||||||||||||||||||||||:||||:||||||||||||||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGWVFGGGTKLTVLG 111

RESULT 8
L1HUBL
Ig lambda chain precursor V-I region (BL2) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
A;Accession: A01966
A;Molecule type: mRNA
A;Residues: 1-130 <TSU>
A;Accession: A01966
R;Tsujimoto, Y.; Croce, C.M.
Nucleic Acids Res. 12, 8407-8414, 1984
A;Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.
A;Reference number: A01966; MUID:85062823; PMID:6095199
A;Cross-references: UNIPROT:P06316; GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087
A;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Comment: Ig lambda chain V-I region (BL2) #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-130/Product: Ig lambda chain V-I region (BL2) #status predicted <MAT>
F;20-115/Region: V segment
F;116-130/Region: J segment
F;34-110/Domain: immunoglobulin homology <IMM>
F;41-108/Disulfide bonds: #status predicted

Query Match   89.2%; Score 523; DB 1; Length 130;
Best Local Similarity   90.1%; Pred. No. 7.1e-38;
Matches 100; Conservative   5; Mismatches   6; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSVSPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Db   20 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLG 79

Qy   1 QSVLTQPPSVSVSPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 60
          |||||||||||| |||||||||||||||||||:|||||||||||||||:||||||||||||
Db   1 QSVLTQPPSVSAAPGQEVTISCSGSGSSSNIGNDVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy   ...

Db   80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTKLTVLG 130

RESULT 9
S19664
Ig lambda chain V region (clone alpha-phOx15) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
A;Accession: S19664
A;Molecule type: mRNA
A;Residues: 1-111 <MAR>
A;Cross-references: EMBL:X61641
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19664
A;Molecule type: mRNA
A;Residues: 1-111 <MAR>
A;Cross-references: EMBL:X61641
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24444
A;Molecule type: mRNA
A;Residues: 1-110, 'W' <JON>
A;Cross-references: EMBL:X61641; NID:g35458; PIDN:CAA433822.1; PID:g1335271
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-91/Domain: immunoglobulin homology <IMM>

Query Match   89.2%; Score 520; DB 2; Length 111;
Best Local Similarity   89.2%; Pred. No. 1.1e-37;
Matches 99; Conservative   3; Mismatches   9; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSVSPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 60
          |||||||||||| |||||||||||||||||||:|||||||||||||||:||||||||||||
Db   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNDVSWYQQLPGTAPNLLIYDNNKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
          |||||||||||||||||||||||||||||||:||||:||||||||||||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGWVFGGGTKLTVLG 111

RESULT 10
L1HUNW
Ig lambda chain V-I region (New) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
A;Accession: A01964
A;Molecule type: protein
A;Residues: 1-111 <LAN>
A;Accession: A01964
R;Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A;Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg
A;Reference number: A01964; MUID:69060892; PMID:4177823
A;Cross-references: UNIPROT:P01701
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGLV@
C;Cross-references: GDB:119342; OMIM:147240
C;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer <IMM>
F;15-91/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-89/Disulfide bonds: #status predicted

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60

RESULT 11

```
Qy    1 QSVLTQPPSVSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 QSVLTQPPSVSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
        |||||||||||||||||:||||||||||||||||||||||||||||||||
Db   61 DRISASKSGTSATLGITGLRTGDEADYYCATWDSSLNAVVPGGGTKVTVLG 111
```

Query Match   86.7%;   Score 508;   DB 1;   Length 111;
Best Local Similarity   86.5%;   Pred. No. 1.2e-36;
Matches 96;   Conservative   7;   Mismatches   8;   Indels   0;   Gaps   0;

S47185

Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
A;Accession: S47185
A;Molecule type: mRNA
A;Residues: 1-111 <MCI>
A;Cross-references: EMBL:X79782; NID:g506428; PIDN:CAA56178.1; PID:g506429
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>
A;Accession: S47181
A;Reference number: S47185
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
submitted to the EMBL Data Library, June 1994
R;Williams, S.C.
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

RESULT 12

```
Qy    2 SVLTQPPSVSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIPD 61
        |||||:|||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db    1 SELTQPPSVSVSAAPGQRVTISCSGSGSSNIGKNYVSWYQQLPGTAPKLLIYKNNKRPSGIPD 60

Qy   62 RFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA-VVPGGGTKLTVL 110
        ||||||||||||||:|||||||||||||||||||||| :||||||||||
Db   61 RFSGSKSGTSATLGITRLQTGDEADYYCGTWDSSLSGGCRGIPGGGTKLTVL 111
```

Query Match   82.9%;   Score 486;   DB 2;   Length 111;
Best Local Similarity   86.5%;   Pred. No. 8.7e-35;
Matches 96;   Conservative   3;   Mismatches 10;   Indels   2;   Gaps   1;

S36050

Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
A;Accession: S36050
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22191; NID:g312298; PIDN:CAA80201.1; PID:g312299
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>
A;Status: preliminary
A;Accession: S36050
A;Reference number: S36046
submitted to the EMBL Data Library, April 1993

RESULT 13

```
Qy    1 QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   18 QSVLTQPPSVSASGTPGQRVTISCSGSGSSNIGSNTVNWYQQLPGTAPKLLIYRNNRPSGVP 77

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
        |||||||||||||:|||||:||||||||||||||||||||||||||||||||||
Db   78 DRFSGSKSGTSASLAISGLQSEDEADYYCAAWDSLNGVVFGGGTKLTVLGQPK 131
```

Query Match   82.8%;   Score 485;   DB 2;   Length 233;
Best Local Similarity   79.8%;   Pred. No. 2.2e-34;
Matches 91;   Conservative   9;   Mismatches 14;   Indels   0;   Gaps   0;

S25752

Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
A;Accession: S25752
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>
A;Accession: S25752
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
Eur. J. Immunol. 21, 1513-1522, 1991
R;Combriato, G.; Klobeck, H.G.

RESULT 14

```
Qy    1 QSVLTQPPSVSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 QSVLTQPPSASGTPGQRVTISCSGSGSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVP 79

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
        |||||||||||:|||:|||||||||||||||||||||||:|||||||||||
Db   80 DRFSGSKSGTSATLGITGLQTGDEADYYCCXTWDSSLSGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVP 111
```

Query Match   81.4%;   Score 477;   DB 2;   Length 130;
Best Local Similarity   80.2%;   Pred. No. 6e-34;
Matches 89;   Conservative 10;   Mismatches 12;   Indels   0;   Gaps   0;

S78057

Ig lambda chain precursor V-J region (clone mAB 61VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
A;Accession: S78057; S23722
A;Molecule type: mRNA
A;Residues: 20-130 <HAR>
A;Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;34-110/Domain: immunoglobulin homology <IMM>
A;Accession: S23722
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
R;Harindranath, N.
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notckins
Int. Immunol. 3, 865-875, 1991
A;Accession: S78057; S23722
A;Reference number: S78057; S78051
submitted to the EMBL Data Library, August 1990

Db　　　　80　DRFSGSKSGTSASLAISGLRSEDEADYYCATWDDSLSAVIFGGGTKLTVLG 130

RESULT 15
A42193
Ig lambda chain (BJP-DIA) - human
N;Alternate names: amyloid fibril protein Al-DIA; Bence Jones protein; Ig lambda chain C
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jan-2000
C;Accession: A42193; S18297
R;Klafki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N.
Biochemistry 31, 3265-3272, 1992
A;Title: Complete amino acid sequence determinations demonstrate identity of the urinary
A;Reference number: A42193; MUID:92207944; PMID:1554711
A;Accession: A42193
A;Molecule type: protein
A;Residues: 1-216 <KLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match　　　80.9%;　Score 474;　DB 2;　Length 216;
Best Local Similarity　　77.2%;　Pred. No. 1.8e-33;
Matches　88;　Conservative　11;　Mismatches　15;　Indels　0;　Gaps　0;

Qy　　1　QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
　　　　　||||||||||||| ::||||||||||||:||:||||||||||||||| :|||||:|
Db　　1　QSVLTQPPSASGTPGQRVTISCSGSSSSNIGSNVVTWYQQLPGTAPKLLIYTNNQRPSGVP 60

Qy　　61　DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVFGGGTKLTVLGQPK 114
　　　　　 ||||||||||||: :||||||| ||| |:: |||||||||||||||||||||
Db　　61　GRFSGSKSGTSASLAVSGLQSEDEADYYCATWDDSVNGWVRGGGTKLTVLGQPK 114

Search completed: October 13, 2005, 03:11:47
Job time : 24.485 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 13, 2005, 02:44:40 ; Search time 117.425 Seconds
                                                     (without alignments)
                                                     375.480 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI..........SLSAVVFGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
                      Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   1_A_Geneseq_16Dec04:*
                2: geneseqp1980s:*
                3: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                        SUMMARIES

                         %
Result   Query
No.   Score   Match Length DB ID   Description
----- -----   ----- ------ -- --------   -----------
  1   582   99.1   114   5   Abb07187   sHigM22 l
  2   582   99.3   114   5   Abb07170   sHigM22 1
  3   582   99.3   114   8   Adi26656   Human ant
  4   547.5   93.4   234   6   Abm84293   Human dia
  5   544   92.8   234   8   Abg73422   Human IgG
  6   543   92.7   111   8   Abg75338   Human IgG
  7   543   92.0   234   7   Aae39158   IgG3 anti
  8   539   92.0   248   8   Ads09288   Human c-M
  9   538   91.8   111   2   Aar12263   Anti-huma
 10   538   91.8   243   6   Aao31147   Human CMO
 11   537.5   91.7   234   8   Abm84291   Human dia
 12   537   91.6   110   8   Adp22405   Human ant
 13   537   91.6   110   8   Adp22403   Human ant
 14   534   91.1   258   5   Abp45249   Human Bly
 15   534   91.1   258   7   Adg96076   Single ch
 16   533   91.0   248   7   Abp45235   Human Bly
 17   533   91.0   248   7   Adg96062   Single ch
 18   532   90.8   112   6   Abr55778   Lambda ch
 19   530   90.4   255   6   Abp45145   Human Bly
 20   530   90.4   255   7   Adg95972   Single ch
 21   528.5   90.2   212   8   Abm84288   Human ant
 22   528   90.1   108   8   Aao18432   Human dia
 23   528   90.1   110   8   Adp22258   Anti-GD2
 24   528   90.1   110   8   Adp22180   Human ant
 25   528   90.1   248   5   Abp44850   Human Bly
 26   528   90.1   248   7   Adg95677   Single ch
 27   528   90.1   248   8   Ads09259   Human c-M
 28   528   90.1   251   5   Abp45540   Human Bly
 29   528   90.0   251   7   Adg96367   Single ch
 30   527.5   90.0   111   5   Abr55774   Lambda ch
 31   526   89.8   111   5   Aao18430   Anti-GD2
 32   526   89.8   253   5   Abp45848   Human Bly
 33   524   89.4   262   7   Adg96675   Single ch
 34   524   89.2   253   7   Adh44200   sFv antib
 35   523   89.2   251   7   Adg30494   Human GMC
 36   522   89.1   244   5   Ads09242   Human c-M
 37   522   89.1   248   5   Abp45454   Human Bly
 38   522   89.1   248   7   Adg96281   Neurokinl
 39   522   89.1   248   8   Adg34302   Neurokinl
 40   522   89.1   251   5   Abp45527   Human Bly
 41   522   89.1   251   7   Adg96354   Single ch
 42   522   89.1   256   5   Abp45004   Human Bly
 43   522   89.1   256   7   Adg95831   Single ch
 44   521   88.9   109   5   Aao18435   Anti-GD2
 45   521   88.9   123   6   Aao19680   P aerugin

                                      ALIGNMENTS

RESULT 1
ABB07187

ID   ABB07187 standard; protein; 114 AA.
XX
AC   ABB07187;
XX
DT   13-MAR-2002 (first entry)
XX
DE   sHigM22 light chain variable region clone II amino acid sequence.
XX
KW   Neuromodulatory; central nervous system; CNS; sHigM22; LYM 22; AKUR4;
KW   ebvHigM Ms119D10; ebv HigM CB2bG8; CB2iE12; CB2iE7; MS119E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS   Homo sapiens.
XX
PN   WO200185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US014902.
XX
PR   10-MAY-2000; 2000US-00568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M, Miller DJ, Pease LR;
XX
DR   WPI; 2002-066596/09.
DR   N-PSDB; ABA94244.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT   neurite outgrowth, regeneration, remyelination and neuroprotection in
PT   central nervous system, useful to treat post-infectious
PT   encephalomyelitis.
XX
PS   Claim 23; Fig 18; 219pp; English.
XX
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHigM22 (LYM 22), ebvHigM MS119D10, ebv HigM
CC   CB2bG8, AkUR4, CB2iE12, CB2iE7 or MS119E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within

```
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture. (I)
CC   is also useful for preventing infection by a bacterium, virus or like
CC   pathogen that causes demyelination or other neurodegenerative condition
CC   in a subject. Methods where (I) is administered to a patient are useful
CC   for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC   disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC   disease, CNS diseases, and other conditions in the CNS where nerves are
CC   damaged as by trauma. The present sequence represents the sHigM22 light
CC   chain variable region clone II amino acid sequence
XX
SQ   Sequence 114 AA;

Query Match             99.3%;  Score 582; DB 5; Length 114;
Best Local Similarity   98.2%;  Pred. No. 8.8e-41;
Matches  112;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1 QSVLTQPPSVSVSAAPGQKVTISCSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          |||||||||| ||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    1 QSVLTQPPSVSAAPGQKVTISCSGSSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCETWDSSLSAVVFGGGTKLTVLGQPK 114

RESULT 2
ID   ABB07170 standard; protein; 114 AA.
XX
AC   ABB07170;
XX
DT   13-MAR-2002  (first entry)
XX
DE   sHigM22 light chain variable region clone I amino acid sequence.
XX
KW   Neuromodulatory; central nervous system; CNS; sHigM22; LYM 22; AKGR4;
KW   ebvHigM Ma1l9D10; ebv HigM CB2bG8; CB21E12; CB21E7; MSI19E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS   Homo sapiens.
XX
PN   WO020185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US014902.
XX
PR   10-MAY-2000; 2000US-00568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M, Miller DJ, Pease LR;
XX
DR   WPI; 2002-066596/09.
DR   N-PSDB; ABA94217.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT   neurite outgrowth, regeneration, remyelination and neuroprotection in
PT   central nervous system, useful to treat post-infectious
PT   encephalomyelitis.
XX
PS   Claim 23; Fig 18; 219pp; English.
XX
   The invention provides a neuromodulatory agent (I) capable of promoting
   neurite outgrowth, remyelination and neuroprotection in
   central nervous system (CNS). (I) is capable of inducing remyelination,
   promoting cellular proliferation of glial cells, and promoting Ca2+
```

```
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHigM22 (LYM 22), ebvHigM Ma1l9D10, ebv HigM
CC   CB2bG8, AKGR4, CB21E12, CB21E7 or MSI19E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture. (I)
CC   are useful for preventing infection by a bacterium, virus or like
CC   pathogen that causes demyelination or other neurodegenerative condition
CC   in a subject. Methods where (I) is administered to a patient are useful
CC   for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC   disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC   disease, CNS diseases, and other conditions in the CNS where nerves are
CC   damaged as by trauma. The present sequence represents the sHigM22 light
CC   chain variable region clone I amino acid sequence
XX
SQ   Sequence 114 AA;

Query Match             99.3%;  Score 582; DB 5; Length 114;
Best Local Similarity   98.2%;  Pred. No. 8.8e-41;
Matches  112;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    1 QSVLTQPPSVSVSAAPGQKVTISCSGSSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
          |||||||||| |||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    1 QSVLTQPPSVSAAPGQKVTISCSGSSSSNIGNNFVSWYQQLPGTAPRLLIYDITKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQPK 114
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQPK 114

RESULT 3
ID   ADI26656 standard; protein; 114 AA.
XX
AC   ADI26656;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human anti IgM antibody sHigM22 VL protein.
XX
KW   Human; antibody; IgM; remyelination; neuronal growth; autoantibody;
KW   demyelination disease; multiple sclerosis; central nervous system; CNS;
KW   axon; glial cell proliferation;
KW   Theiler's murine encephalomyelitis virus infection; CNS injury;
KW   spinal cord injury.
XX
OS   Homo sapiens.
XX
PN   US2003185827-A1.
XX
PD   02-OCT-2003.
XX
PF   13-NOV-2001; 2001US-00010729.
XX
PR   29-APR-1994; 94US-00236520.
PR   08-AUG-1996; 96US-00692084.
PR   07-JAN-1997; 97US-00779784.
PR   28-MAY-1999; 99US-00322862.
PR   30-MAY-2000; 2000US-00580787.
PR   05-DEC-2000; 2000US-00730473.
XX
PA   (MAYO-) MAYO FOUND.
XX
PI   Rodriguez M, Miller DJ, Pease LR;
XX
DR   WPI; 2004-119219/12.
```

DR   N-PSDB; AD126657.
XX
PT   New human immunoglobulin M antibody for treating or preventing a
PT   demyelinating disease of the central nervous system in a human or
PT   domestic animal, such as multiple sclerosis.
XX
PS   Claim 6; Fig 36; 159pp; English.
XX

The invention relates to an antibody (I) produced by injecting an
immunocompetent host with an antibody peptide, and harvesting the
antibody, where the peptide comprises a human anti-IgM antibody fragment
given in the specification, or active fragments, or mixtures. Also included are
stimulating remyelination of central nervous system (CNS) axons in a
mammal (comprising administering a monoclonal antibody, or mixtures,
monomers, active fragments, or recombinant antibodies derived from it,
characterised by their ability to bind structures and cells within the
CNS, including oligodendrocytes), stimulating the proliferation of glial
cells in CNS axons in a mammal (comprising administering a monoclonal
antibody, or mixtures, monomers, active fragments, or recombinant
antibodies derived from it, characterised by their ability to bind
antibodies and cells within the CNS), treating or preventing a
demyelinating disease of the CNS in a mammal (comprising administering a
monoclonal antibody, or mixtures, monomers, active fragments, or
recombinant antibodies derived from it, characterised by their ability to
bind structures and cells within the CNS, and to stimulate remyelination
of axons of the CNS), stimulating, in vitro, the proliferation of glial
cells from mixed cell culture, stimulating remyelination of CNS axons in
a mammal, a DNA sequence (or degenerate variant of it) which encodes an
antibody(or a peptide analogue, hapten, or active fragment of it, where
the DNA sequence consists of a sequence encoding an anti IgM antibody), a
probe capable of screening for the antibody, an assay for screening drugs
and other agents for the ability to modulate the production or mimic the
activities of mAb sHIgM22, sHIgM46, or combinations of them, a
recombinant virus transformed with recombinant antibody nucleic acids or
vector, imaging a portion of the CNS using the antibody and diagnosing or
monitoring demyelination and/or remyelination of the CNS comprising using
CNS image. The antibody is used to stimulate remyelination of CNS axons,
and to stimulate the proliferation of glial cells in CNS axons,
optionally in vitro. The antibody is used to treat or prevent a
demyelinating disease of the CNS in a human or domestic animal, such as
multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
preferably the mammal is a mouse infected with Strain DA of Theiler's
murine encephalomyelitis virus. The antibody is used to treat a spinal
cord injury and used to screen drugs and other agents for the ability to
modulate the production or mimic the activities of the antibody. The
antibody can be used to image a portion of the CNS which can be used to
diagnose or monitor demyelination and/or remyelination of the CNS. The
present sequence is a variable region of a human anti-IgM antibody (or
fragment).

XX
SQ   Sequence 114 AA;

Query Match   99.3%; Score 582; DB 8; Length 114;
Best Local Similarity   100.0%; Pred. No. 8.8e-41;
Matches 114; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114

RESULT 4
ID   ABM84293
AC   ABM84293;
XX

ABM84293 standard; protein; 234 AA.

DT   18-NOV-2004 (first entry)

DE   Human diagnostic and therapeutic pprotein SEQ ID NO:4542.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
FN   WO200402973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI   Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI   Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI   Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI   Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve L;
PI   Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI   Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI   Patury S, Shi X, Suarez CU;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42945.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX

The invention relates to novel diagnostic and therapeutic polynucleotides
selected from one of the 2722 sequences defined in the specification. A
polynucleotide of the invention may have a use in gene therapy. The human
diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
used to diagnose a particular condition, disease or disorder associated
with human molecules, e.g. cell proliferative disorders,
autoimmune/inflammatory disorder, developmental disorder, endocrine
disorder, neurological disorders, gastrointestinal disorders, or
infections caused by virus, bacteria, fungi or parasite. The dithp
molecules may also be used in genetic mapping, in identifying individuals
from minute biological samples, in detecting single nucleotide
polymorphisms, as molecular weight markers, and for somatic or germline
gene therapy. The present sequence represents a dithp protein of the
invention. Note: The sequence data for this patent is not represented in
the printed specification, but was obtained in electronic format directly
from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 234 AA;

Query Match   93.4%; Score 547.5; DB 8; Length 234;
Best Local Similarity   93.9%; Pred. No. 1.3e-37;
Matches 107; Conservative   1; Mismatches   5; Indels   1; Gaps   1;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||| |||||||||||||||||||||||| |||||||
Db   20 QSVLTQPPSVSAAPGQKVTISCSGSGSSNIGNNFVSWYQQLPGTAPXLLIYDNNRPSGIP 79

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSL-MVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSL-MVFGGGTKLTVLGQPK 132

RESULT 5
ID   ABG73422
AC   ABG73422;
XX

ABG73422 standard; protein; 234 AA.

DT 24-APR-2003 (first entry)
XX
DE Human IgG anti-rhesus antibody lambda light chain polypeptide.
XX
KW IgG anti-rhesus antibody; Rh; gamma 3 heavy chain; lambda light chain;
KW haemagglutinin; rhesus antigen; red blood cell; agglutination; antibody;
KW Rh phenotyping; human.
XX
OS Homo sapiens.
XX
PN US6475749-B1.
XX
PD 05-NOV-2002.
XX
PF 11-AUG-1999; 99US-0037242425.
XX
PR 11-AUG-1999; 99US-0037242425.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Morrison SL, Montano R;
XX
DR WPI; 2003-208833/20.
DR N-PSDB; ABX15392.
XX
PT Claim 1; Col 13-16; 14pp; English.
XX
PS The invention relates to a reagent comprising an IgG anti-Rh antibody
CC having two lambda light chains, two gamma 3 heavy chains and a polymeric
CC tailpiece attached to the carboxy terminal end of the heavy chain. The
CC reagent is useful in a haemagglutinin test to determine the presence of
CC one or more Rh (rhesus) antigens on red blood cells. The reagent is also
CC useful for testing red blood cells to determine the presence of one or
CC more Rh factors, by contacting red blood cells with the reagent for a
CC sufficient time and at a sufficient temperature to cause agglutination of
CC red blood cells which have one or more Rh factors present, and
CC determining whether the red blood cells agglutinate to determine the
CC presence of one or more Rh factors. The reagent allows fast and accurate
CC Rh phenotyping of blood and is used in the one-step haemagglutinin
CC method. This sequence represents a human IgG anti-Rh antibody lambda
CC light chain polypeptide
XX
SQ Sequence 234 AA;

Query Match 92.8%; Score 544; DB 6; Length 234;
Best Local Similarity 90.4%; Pred. No. 2.5e-37;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```
Qy    1 QSVLTQPPSVSVAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
         |||||||||||||||||||||||||||||||||||||||| ||||||| ::||||||||||
Db   19 QSVLTQPPSVSAAPGQKVTISCSGSGSSSNIGNNYVSWYQHFPGTAPKLLIYDNNQRPSGIP 78

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
         |||||||||||||||||||||||||||||||:||||||::||||||||||||
Db   79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVLPGGGTKTEVTVLGQPK 132
```

XX
KW Antibody; framework; stability; intracellular; Fv; solubility.
XX
OS Synthetic.
XX
PN WO2003097697-A2.
XX
PD 27-NOV-2003.
XX
PF 21-MAY-2003; 2003WO-EP005324.
XX
PR 22-MAY-2002; 2002US-0382649P.
PR 03-JAN-2003; 2003US-0438256P.
XX
PA (ESBA-) ESBATECH AG.
XX
PI Tissot K, Ewert S, Auf Der Maur A, Barberis A, Escher D;
XX
DR WPI; 2004-022852/02.
XX
PT New single chain immunoglobulin frameworks that demonstrate enhanced
PT stability in the intracellular environment, useful for target validation,
PT library construction, or in therapeutic or diagnostic applications.
XX
PT Claim 6; Page 48; 0pp; English.
XX
CC The present invention relates to a single chain antibody framework. The
CC single chain framework, antibody or antibody fragment, is useful in
CC target validation, diagnostic applications, library construction or
CC therapeutic applications. The framework sequences are used in the
CC identification of a conserved framework residue class selected from polar
CC but uncharged R groups, positively charged R groups, negatively charged R
CC groups, hydrophobic R groups, and special amino acids. The framework
CC sequences may also be used in the identification of at least one
CC conserved framework sequence, where the conserved framework sequence is 2
CC -5, 5-10 or 10-25 residues, and where the conserved framework sequence
CC has gaps. The nucleic acid molecule is used in gene therapy. The present
CC sequence is a polypeptide of the invention
XX
SQ Sequence 111 AA;

Query Match 92.7%; Score 543; DB 8; Length 111;
Best Local Similarity 93.7%; Pred. No. 1.5e-37;
Matches 104; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy    1 QSVLTQPPSVSVAAPGQKVTISCSGSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
         |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db    1 QSVLTQPPSVSAAPGQKVTISCSGSGSTSNIGDNYVSWYQQLPGTAPQLLIYDNTKRPSGIP 60

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
         ||||||||||||||||||||||||||||||||||||||:||||||||||||
Db    1 QSVLTQPPSVSAAPGQKVTISCSGSGSTSNIGDNVVSWYQQLPGTAPQLLIYDNTKRPSGIP 60
```

ABG75338
ID ABG75338 standard; protein; 111 AA.
XX
AC ABG75338;
XX
DT 22-APR-2004 (first entry)
XX
DE Antibody single chain framework polypeptide SEQ ID NO: 4.
XX
KW Anti-rhesus antibody; Rh; immunoglobulin G; IgG; haemagglutinin test;
KW Rh phenotyping; therapeutic; haemolytic disease; Rh incompatibility;
KW prophylactic.
XX
OS Unidentified.
XX
FH Key   Location/Qualifiers
FT Misc-difference 111
FT   /note= "Encoded by GAT"
XX

AAB39158
ID AAB39158 standard; protein; 234 AA.
XX
AC AAB39158;
XX
DT 18-DEC-2003 (first entry)
XX
DE IgG3 antibody lambda light chain protein.
XX
KW Anti-rhesus antibody; Rh; immunoglobulin G; IgG; haemagglutinin test;
KW Rh phenotyping; therapeutic; haemolytic disease; Rh incompatibility;
KW prophylactic.
XX

PN   US2003143643-A1.
XX
PD   31-JUL-2003.
XX
PF   12-JUL-2002; 2002US-00194801.
XX
PF   11-AUG-1999; 99US-00372425.
XX
PR   (REGC) UNIV CALIFORNIA.
XX
PA
PI   Morrison SL, Montano R;
XX
DR   WPI; 2003-755510/71.
DR   N-PSDB; AAD59473.
XX
PS   Claim 7; Page 8-9; Opp; English.
XX
PT   Hybrid immunoglobulin G anti-Rhesus antibody for use in one-step Rh
PT   phenotyping of blood or as a prophylactic agent to prevent hemolytic
PT   disease in newborns due to Rh incompatibility, comprises a polymeric
PT   carboxy terminus tailpiece.
XX
CC   The invention relates to hybrid anti-Rhesus (Rh) antibody comprising an
CC   immunoglobulin (Ig)G anti-Rh antibody which comprises two light chains
CC   and two heavy chains where the heavy chains have a carboxy terminal with
CC   a polymeric tailpiece and an amino terminal. The antibodies are used in a
CC   one-step haemagglutinin test to provide Rh phenotyping of blood and as
CC   therapeutic or prophylactic agents for preventing haemolytic disease in
CC   newborns due to Rh incompatibility. The present sequence is IgG3 antibody
CC   lambda light chain protein
XX
SQ   Sequence 234 AA;

Query Match   92.0%; Score 539; DB 7; Length 234;
Best Local Similarity   89.5%;
Matches 102; Conservative   6; Mismatches   6; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSVAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||||||||||| ||||||||:|||||||||||||
Db   19 QSVLTQPPSVSVAAPGQKVTISCSGSSSNIGNNYVSWYQHFPGTAPKLLIYDNNQRPSGIP 78

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              ||||||||||||||||:|||||||||||||||||| :||||||||||||||||
Db   79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNSSLSAVLFGGGTEVVTVLGQPK 132

PA   (PHAA) PHARMACIA CORP.
XX
PI   Morton PA, Arbuckle JA, Evans ML, Joy WD, Kahn LE, Shieh JJ;
XX
DR   WPI; 2004-616044/59.
DR   N-PSDB; ADS09348.
XX
PS   Claim 1; SEQ ID NO 50; 303pp; English.
XX
PT   Novel c-Met protein tyrosine kinase antibody or its antigen-binding
PT   portion specifically binding to c-Met, useful for manufacture of
PT   medicament for treating cancer or tumor and for treatment of ophthalmic
PT   diseases such as glaucoma.
XX
CC   The invention relates to a novel c-Met protein tyrosine kinase antibody
CC   or its antigen binding portion that specifically binds to c-Met. The c-
CC   Met antibody comprises any one of 1-60 fully defined sequence of 238,
CC   244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc.; amino
CC   acids as given in the specification, or its fragment. The invention
CC   further comprises: a pharmaceutical composition comprising the c-Met
CC   protein tyrosine kinase antibody and a carrier; an isolated cell that
CC   produces the c-Met protein tyrosine kinase antibody; and an isolated
CC   nucleic acid molecule that comprises a nucleic acid sequence that encodes
CC   a heavy chain or its antigen-binding portion or light chain or its
CC   antigen-binding portion of the c-Met protein tyrosine kinase antibody.
CC   The c-Met protein tyrosine kinase antibody has cytostatic,
CC   ophthalmological, antiinflammatory, analgesic, vasotropic, antipsoriatic,
CC   and osteopathic activities. The c-Met protein tyrosine kinase antibody is
CC   useful for the manufacture of medicament for the treatment of cancer or
CC   tumour. The c-Met protein tyrosine kinase antibody is useful for
CC   diagnosing the presence or ligation of c-Met expressing tissue. The c-Met
CC   protein tyrosine kinase antibody is useful for detecting c-Met in a
CC   biological sample in vitro or in vivo. The c-Met protein tyrosine kinase
CC   antibody is also useful in the treatment or prevention of ophthalmic
CC   diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic
CC   retinopathy), uveitis, ocular photophobia, macular degeneration and pain
CC   associated with acute injury to the eye. The pharmaceutical composition
CC   is useful for the treatment of hyperproliferative disorders such as
CC   restenosis after angioplasty, and psoriasis, and for the treatment of
CC   animals that lack sufficient HGF, e.g. osteoporosis and cancer. This
CC   sequence represents the protein of a phage display generated human c-Met
CC   antibody of the invention.
XX
SQ   Sequence 248 AA;

Query Match   92.0%; Score 539; DB 8; Length 248;
Best Local Similarity   92.8%;
Matches 103; Conservative   3; Mismatches   5; Indels   0; Gaps   0;

Qy   1 QSVLTQPPSVSVAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||||||||||||| ||:|||||||:|||||||||
Db   138 QSVVTQPPSVSVAAPGQKVTISCSGSSSNIGNNVVSWYQLPGTAPKLLIYDNNKRPSGIP 197

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||:||||||||||||||| :||||||||||||||
Db   198 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGVVFGGGTKLTVLG 248

DT   18-NOV-2004 (first entry)
XX
DE   Human c-Met protein tyrosine kinase antibody, PGIA-4-A3.
XX
KW   c-Met; tyrosine kinase antibody; antigen binding; cytostatic;
KW   ophthalmological; antiinflammatory; analgesic; vasotropic; antipsoriatic;
KW   osteopathic; cancer; tumour; ophthalmic disease; glaucoma; retinitis;
KW   retinopathy; uveitis; ocular photophobia; glaucoma; retinitis;
KW   acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;
KW   psoriasis; HGF; osteoporosis; cancer.
XX
OS   Homo sapiens.
XX

RESULT 8
ID   ADS09288 standard; protein; 248 AA.
XX
AC   ADS09288;
XX
DT   18-NOV-2004 (first entry)

RESULT 9
ID   AAR12263 standard; protein; 111 AA.
XX
AC   AAR12263;
XX
DT   25-MAR-2003 (revised)
DT   15-AUG-1991 (first entry)
XX
DE   Anti-human RhD FOG-B MAb (VL chain).
XX
KW   Monoclonal antibody; rhesus D; blood-typing; CDR;
KW   haemolytic disease of the newborn; HDN.
XX
OS   Homo sapiens.

PN   US2004072117-A2.
XX
PD   26-AUG-2004.
XX
PF   WO200407211 7-A2.
XX
PF   11-FEB-2004; 2004WO-IB000503.
XX
PR   13-FEB-2003; 2003US-0447073P.
XX

OS   Homo sapiens.

Left column:

```
FH   Key                Location/Qualifiers
FT   Region             23..35
FT                      /label= CDR1
FT   Region             51..57
FT                      /label= CDR2
FT   Region             90..100
FT                      /label= CDR3
XX
PN   WO9107492-A.
XX
PD   30-MAY-1991.
XX
PF   13-NOV-1989;    89GB-00025590.
XX
PR   13-NOV-1989;    89GB-00025590.
XX
PA   (BLOO-) CENT BLOOD LAB AUTHORITY.
XX
PI   Hugheejone N;
XX
DR   WPI; 1991-178104/24.
DR   N-PSDB; AAQ11945.
XX
PT   DNA encoding complementary determining regions - of human anti-rhesus d
PT   antibodies, useful in prodn. of monoclonal antibodies and for passive
PT   immunisation.
XX
PS   Disclosure; Fig 2; 32pp; English.
XX
CC   The DNA sequence of eleven monoclonal antibodies are represented in
CC   Q19145-57. Synthetic genes, for both heavy and light chains may be
CC   created by combining selected CDR 1, 2, and 3 regions, which may be
CC   selected from different antibody mols. having varied binding specificity.
CC   The chimaeric anti-RhD antibodies can be used for diagnosis and therapy,
CC   and are capable of providing blood- typing reagents of high specificity
CC   and reliability. They can also be used in passive immunisation to prevent
CC   haemolytic disease of the newborn. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 111 AA;
```

```
Qy    Best Local Similarity   91.8%;   Score 538;   DB 2;   Length 111;
      Query Match
      Matches 103;   Conservative   93.6%;   Pred. No. 3.8e-37;   Mismatches   4;   Indels   0;   Gaps   0;

Qy     1  QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP  60
          ||||||||||||||||||||||||||||||||||:||||||||||||:||||||||||||
Db     1  QSVLTQPPSVSAAPGQKVTISCSGSTSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP  60

Qy    61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL  110
          |||||||||||||||||||||:|||||||||:|||||||||||||||||
Db    61  DRFSGSKSGTSATLGITGLRTGDBADYYCATWDSSLSAVVFGGGTKLTVL  110
```

Right column:

```
XX
OS   Homo sapiens.
XX
PN   WO2003054216-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002;    2002WO-US040597.
XX
PR   20-DEC-2001;    2001US-0341237P.
PR   05-APR-2002;    2002US-0369877P.
PR   04-JUN-2002;    2002US-0384828P.
PR   18-JUL-2002;    2002US-0396591P.
PR   13-AUG-2002;    2002US-0403370P.
PR   13-NOV-2002;    2002US-0425737P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
XX
DR   WPI; 2003-569250/53.
DR   N-PSDB; AAL62844.
XX
PT   New antibody or its fragment, useful for treating, preventing or
PT   ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
PT   gastrointestinal cancer, or Kaposi's sarcoma or graft versus host
PT   disease, AIDS.
XX
PS   Claim 2; Page 288; 301pp; English.
XX
CC   The invention relates to an isolated antibody or its fragments such as
CC   VHCDR1 (heavy chain variable domain complementarity determining region),
CC   VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
CC   determining region), VLCDR2 or VLCDR3. The antibody or its fragment
CC   immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
CC   apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
CC   TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
CC   antibody or its fragment is useful for treating, preventing or
CC   ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
CC   gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
CC   nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
CC   graft versus host disease, AIDS (acquired immune deficiency syndrome) or
CC   a neurodegenerative disorder. The invention is useful in antibody
CC   therapy. The present sequence is human scFv protein that specifically
CC   binds TR7
XX
SQ   Sequence 243 AA;
```

```
Qy    Best Local Similarity   91.8%;   Score 538;   DB 6;   Length 243;
      Query Match
      Matches 102;   Conservative   91.9%;   Pred. No. 8.3e-37;   Mismatches   4;   Indels   0;   Gaps   0;

Qy     1  QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP  60
          ||||||||||||||||||||||||||||||||||:||||||||||||:||||||||||||
Db   133  QSVLTQPPSVSAAPGQKVTISCSGSTSSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP  192

Qy    61  DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG  111
          |||||||||||||||||||||:|||||||||:||||||||||:||||||||
Db   193  DRFSGSKSGTSATLGITGLRTGDBADYYCGTWDSSLSAIVFGGGTKVTVLG  243
```

RESULT 10

```
AC   AAO31147
XX
ID   AAO31147 standard; protein; 243 AA.
XX
AC   AAO31147;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human CM08SC11 scFv protein that specifically binds TR7.
XX
KW   Human; protein coordinate data; heavy chain variable domain; VH; cancer;
KW   complementarity determining region; CDR; light chain variable domain; VL;
KW   TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
KW   DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
KW   Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
KW   glioblastoma; graft versus host disease; antibody therapy; neotropic;
KW   AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
KW   immunosuppressive; neuroprotective; antibody therapy; antibody.
```

RESULT 11

```
AC   ABM84291
XX
ID   ABM84291 standard; protein; 234 AA.
XX
AC   ABM84291;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:4540.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
```

Left column

```
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P;
PI   Harthshorne RS, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI   Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI   Stevens KA, Blanchard JT, Panzer SR, Wang X, Au AP, Gerstin EH;
PI   Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;
PI   Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI   Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI   Patury S, Shi X, Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN42943.
XX
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorders, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 234 AA;

Query Match             91.7%;  Score 537.5;  DB 8;  Length 234;
Best Local Similarity   92.1%;  Pred. No. 8.8e-37;
Matches 105;  Conservative  2;  Mismatches  6;  Indels  1;  Gaps  1;

Qy      1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db     20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 79

Qy     61 DRFSGSKSGTSATLGITGLQTGDEADYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
          |||||||||||||||||||||||||||  ||||  ||| |||||||||||||||
Db     80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSL-MLGFGGGTKLTVLGQPK 132
```

Right column

```
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis.
XX
XX
OS   Homo sapiens.
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcook JS, Kang JS, Foord O, Green L, Peng X, Klakamp S;
PI   Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI   Manchulenono K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
XX
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 311; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two-fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421)
CC   and-(b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence represents a human anti-TNFa
CC   antibody light chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 110 AA;

Query Match             91.6%;  Score 537;  DB 8;  Length 110;
```

Bottom section

```
RESULT 12
AC   ADP22405
ID   ADP22405 standard; protein; 110 AA.
XX
AC   ADP22405;
XX
DT   09-SEP-2004 (first entry)
XX
DE   Human anti-TNFA antibody light chain variable region SEQ ID NO:311.
```

Best Local Similarity 94.5%; Pred. No. 4.6e-37;
Matches 104; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
        ||||||||||||||||||||||||||||||||:||||||||||| ||||||||
Db   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy  61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
        ||||||||||||||||||||||||||||| |||||||:|||||||||
Db  61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110
```

RESULT 13
ID   ADP22403 standard; protein; 110 AA.
XX
AC   ADP22403;
XX
DT   09-SEP-2004 (first entry)
XX
DE   Human anti-TNFa antibody light chain variable region SEQ ID NO:309.
XX
KW   human; monoclonal antibody; anabolic; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   anti-arteriosclerotic; antiarthritic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2002; 2002US-0430729P.
XX
PR   02-DEC-2003; 2003WO-US038281.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI   Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI   Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 309; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, and or immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced

CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (II) has anabolic, antiinflammatory, antipsoriatic, antirheumatic,
CC   antibacterial, antiinflammatory, antiarteriosclerotic, antiarthritic,
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic, and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (II) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer
CC   pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, septic shock, cachexia, anorexia, and
CC   disease, graft-host reactions, autoimmune disease, Crohn's
CC   multiple sclerosis. The present sequence represents a human anti-TNFa
CC   antibody light chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 110 AA;

Query Match 91.6%; Score 537; DB 8; Length 110;
Best Local Similarity 94.5%; Pred. No. 4.6e-37;
Matches 104; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60
        ||||||||||||||||||||||||||||||||:||||||||||| ||||||||
Db   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy  61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
        ||||||||||||||||||||||||||||| |||||||:|||||||||
Db  61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110
```

RESULT 14
ID   ABP45249 standard; protein; 258 AA.
XX
AC   ABP45249;
XX
DT   19-AUG-2002 (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1260.
XX
KW   BLyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO2002024641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HGMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.

XX
PS Claim 1; Page 1906-1907; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptide. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 258 AA;

Query Match   91.1%; Score 534; DB 5; Length 258;
Best Local Similarity   92.8%; Pred. No. 1.9e-36;
Matches 103; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
         |||||||||||||||||||||||||||||||| ||||||||||| ||||| |||||||||
Db 148 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 207

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
         ||||||||||||||||||||||||||||| ||||||||||| |||||||||
Db 208 DRFSGSKSGTSATLGITGLQTGDEADYYCGAWDSSLSAVVFGGSGTKLTVLG 258

RESULT 15
ADG96076
ID ADG96076 standard; protein; 258 AA.
XX
AC ADG96076;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds BLyS SeqID 1260.
XX
KW antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO020305979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (BLyS), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX

PS Example 1; SEQ ID NO 1260; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey BLyS. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of BLyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be degcribed as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BLyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ Sequence 258 AA;

Query Match   91.1%; Score 534; DB 7; Length 258;
Best Local Similarity   92.8%; Pred. No. 1.9e-36;
Matches 103; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy   1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db 148 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 207

Qy   61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
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Db 208 DRFSGSKSGTSATLGITGLQTGDEADYYCGAWDSSLSAVVFGGSGTKLTVLG 258

Search completed: October 13, 2005, 03:06:57
Job time : 119.425 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: October 13, 2005, 02:43:55 ; Search time 115.425 Seconds
                            (without alignments)
                            428.900 Million cell updates/sec

Title: US-10-010-729A-7
Perfect score: 615
Sequence: 1 QVQLVESGGGVVQPGRSLRL.........VTGSPTLDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 41601S017 residues

Total number of hits satisfying chosen parameters: 1854112

Post-processing: Minimum Match 0%
Maximum Match 100%
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Listing first 45 summaries

Database :   Published Applications_AA.*
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                3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
               10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
               11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
               12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
               13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
               14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
               15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
               16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
               17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
               18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
               19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
               20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
               21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
               22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	611	99.3	119	14	US-10-010-729-7	Sequence 7, Appli
2	544	88.5	123	14	US-10-269-805-21	Sequence 21, Appl
3	542.5	88.2	248	14	US-10-235-175-80	Sequence 80, Appl
4	540.5	87.9	120	15	US-10-371-942-18	Sequence 18, Appl
5	540.5	87.9	121	17	US-10-726-332-23	Sequence 23, Appl
6	540	87.8	121	17	US-10-727-155-190	Sequence 190, App
7	540	87.8	123	15	US-10-292-088-115	Sequence 115, App
8	539	87.6	119	14	US-10-120-377-76	Sequence 76, Appl
9	539	87.6	119	17	US-10-980-815-78	Sequence 78, Appl
10	539	87.6	119	18	US-10-992-196-76	Sequence 76, Appl
11	538.5	87.6	241	17	US-10-935-290-100	Sequence 100, App

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

12	538	87.5	113	10	US-09-791-153A-63	Sequence 63, Appl
13	537	87.3	121	20	US-11-021-715-57	Sequence 57, Appl
14	537	87.3	117	17	US-10-727-155-92	Sequence 92, Appl
15	535.5	87.1	117	17	US-10-938-355-110	Sequence 110, App
16	535	87.0	244	20	US-11-021-715-59	Sequence 59, Appl
17	535	87.0	117	16	US-11-935-290-55	Sequence 55, Appl
18	535	87.0	519	14	US-10-312-354-19	Sequence 19, Appl
19	534.5	86.9	118	14	US-10-120-377-78	Sequence 78, Appl
20	534.5	86.9	118	17	US-10-980-815-78	Sequence 78, Appl
21	534.5	86.9	118	17	US-10-992-196-78	Sequence 78, Appl
22	534	86.9	117	20	US-11-021-715-58	Sequence 58, Appl
23	533	86.7	117	20	US-11-047-996-89	Sequence 89, Appl
24	532.5	86.6	121	17	US-10-726-332-142	Sequence 142, App
25	532.5	86.6	127	17	US-10-705-689-36	Sequence 36, Appl
26	532	86.5	127	18	US-10-988-360-36	Sequence 36, Appl
27	532	86.5	463	17	US-10-938-355-18	Sequence 18, Appl
28	531.5	86.4	116	14	US-10-309-764-59	Sequence 59, Appl
29	531.5	86.4	135	15	US-10-309-764-3	Sequence 3, Appl
30	531.5	86.3	126	15	US-10-309-766-133	Sequence 133, App
31	530.5	86.3	252	18	US-10-880-748-1627	Sequence 1627, Ap
32	530.5	86.3	124	17	US-10-293-418-1627	Sequence 1627, Ap
33	530.5	86.2	252	15	US-10-725-962-12	Sequence 12, Appl
34	530	86.2	121	17	US-10-293-418-1627	Sequence 1627, Ap
35	529.5	86.1	252	10	US-09-880-748-1519	Sequence 1519, Ap
36	529.5	86.1	252	15	US-10-293-418-1519	Sequence 1519, Ap
37	529	86.1	115	17	US-10-726-332-136	Sequence 136, App
38	529	86.0	124	17	US-10-884-830-35	Sequence 35, Appl
39	528.5	85.9	115	17	US-10-880-744-512	Sequence 512, App
40	528.5	85.9	249	10	US-09-880-748-512	Sequence 512, App
41	528	85.9	249	15	US-10-293-418-512	Sequence 512, App
42	528	85.9	117	17	US-10-638-265-18	Sequence 18, Appl
43	527.5	85.9	125	15	US-10-292-088-107	Sequence 107, App
44	527.5	85.8	116	15	US-10-309-764-9	Sequence 9, Appl
45	527.5	85.8	135	15	US-10-309-764-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-10-010-729-7

; Sequence 7, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-729-7

RESULT 2
US-10-269-805-21
; Sequence 21, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-21

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Query Match             99.3%;  Score 611;  DB 14;  Length 119;
Best Local Similarity   98.3%;  Pred. No. 9.6e-50;
Matches 117;  Conservative  0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy  1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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Db  1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSRKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
       |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLTADDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
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RESULT 3
US-10-235-175-80
; Sequence 80, Application US/10235175
; Publication No. US20030166287A1
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmuth
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID
; TITLE OF INVENTION: TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/10/235,175
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US/09/315,926
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-10-235-175-80

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Query Match             88.2%;  Score 542.5;  DB 14;  Length 248;
Best Local Similarity   87.5%;  Pred. No. 5.6e-43;
Matches 105;  Conservative  5;  Mismatches   9;  Indels   1;  Gaps   1;

Qy  1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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Db 23 QVQLVQSGGGGVVQPGRSLRLSCAASGFTFSSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT----LDYWGQGTLVTVSS 119
       |||||||||||||||||||||||||: ||||||||||:|:  :     ||||||||||||||
Db 83 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 142
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RESULT 4
US-10-371-942-18
; Sequence 18, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-18

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Query Match             87.9%;  Score 540.5;  DB 15;  Length 120;
Best Local Similarity   88.3%;  Pred. No. 4.1e-43;
Matches 106;  Conservative  5;  Mismatches  11;  Indels   1;  Gaps   1;

Qy  1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
       |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||: ||
Db  1 QVQLVQSGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGS----PTLDYWGQGTLVTVSS 119
       |||||||||||||||||||||||||: ||||||||||:  :     ||||||||||||||
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYYGDYALLDYWGQGTLVTVSS 120
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RESULT 5
US-10-726-332-23
; Sequence 23, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Meina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; TITLE OF INVENTION: AND USES THEREOF

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;   FILE REFERENCE: ABGENIX.072A
;   CURRENT APPLICATION NUMBER: US/10/726,332
;   CURRENT FILING DATE: 2003-12-02
;   PRIOR APPLICATION NUMBER: n/a
;   PRIOR FILING DATE:
;   NUMBER OF SEQ ID NOS: 222
;   SOFTWARE: FastSEQ for Windows Version 4.0
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;   SEQ ID NO 23
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-23

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  Best Local Similarity   87.5%;
  Matches  105;   Conservative  4;   Mismatches  10;   Indels  1;   Gaps  1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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Db       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAAIWYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSP-TLDYWGQGTLVTVSS 119
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Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGTGTPGAPDIWGQGTMVTVSS 120
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RESULT 6
US-10-727-155-190
; Sequence 190, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;   APPLICANT: Jaspal S. Kang
;   APPLICANT: John S. Babcook
;   APPLICANT: Orit Foord
;   APPLICANT: Larry Green
;   APPLICANT: Xiao Feng
;   APPLICANT: Scott Klakamp
;   APPLICANT: Mary Haak-Frendscho
;   APPLICANT: Palaniswami Rathanaswami
;   APPLICANT: Craig Pigott
;   APPLICANT: Meina Liang
;   APPLICANT: Rozanne Lee
;   APPLICANT: Kathy Manchulencho
;   APPLICANT: Raffaella Faggioni
;   APPLICANT: Giorgio Senaldi
;   APPLICANT: Qiaojuan Jane Su
;   TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;   TITLE OF INVENTION: FACTOR AND USES THEREOF
;   FILE REFERENCE: ABGENIX.073A
;   CURRENT APPLICATION NUMBER: US/10/727,155
;   CURRENT FILING DATE: 2003-12-02
;   PRIOR APPLICATION NUMBER: 60/430729
;   PRIOR FILING DATE: 2002-12-02
;   NUMBER OF SEQ ID NOS: 320
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 190
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-190

  Query Match      87.8%;   Score 540.5;   DB 17;   Length 121;
  Best Local Similarity   87.6%;
  Matches  106;   Conservative  2;   Mismatches  11;   Indels  2;   Gaps  1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAAIWYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVS 118
           |||||||||||||||||||||||||||| || ||||||  ||:| ||||||||||||||
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARBGDYGGNPYFDYWGQGTLVTVS 120
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Qy     119 S 119
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Db     121 S 121
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RESULT 7
US-10-292-088-115
; Sequence 115, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;   APPLICANT: BEDIAN, VAHE
;   APPLICANT: GLADUE, RONALD P.
;   APPLICANT: CORVALAN, JOSE
;   APPLICANT: JIA, XIAO-CHI
;   APPLICANT: FENG, XIAO
;   TITLE OF INVENTION: ANTIBODIES TO CD40
;   FILE REFERENCE: ABX-PF/3 US
;   CURRENT APPLICATION NUMBER: US/10/292,088
;   CURRENT FILING DATE: 2003-03-14
;   PRIOR APPLICATION NUMBER: 60/348,980
;   PRIOR FILING DATE: 2001-11-09
;   NUMBER OF SEQ ID NOS: 147
;   SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 115
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-115

  Query Match      87.8%;   Score 540;   DB 15;   Length 123;
  Best Local Similarity   86.2%;
  Matches  106;   Conservative  3;   Mismatches  10;   Indels  4;   Gaps  1;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy      61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGS----PTLDYWGQGTLVT 116
           |||||||||||||||||||||||||||| || |||||||||:|    |.|:|||||||||.
Db      61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTTGTYYYYGMDVWGQGTTVT 120
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Qy     117 VSS 119
           |||
Db     121 VSS 123
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RESULT 8
US-10-120-377-76
; Sequence 76, Application US/10120377
; Publication No. US20030176674A1
; GENERAL INFORMATION:
;   APPLICANT: Rosen, Craig, et al.
;   TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
;   FILE REFERENCE: PF112P8
;   CURRENT APPLICATION NUMBER: US/10/120,377
;   CURRENT FILING DATE: 2002-04-12
;   PRIOR APPLICATION NUMBER: 60/283,391
;   PRIOR FILING DATE: 2001-04-13
;   PRIOR APPLICATION NUMBER: 60/317,600
;   PRIOR FILING DATE: 2001-09-07
;   NUMBER OF SEQ ID NOS: 79
;   SOFTWARE: Patentin version 3.1
;
;   SEQ ID NO 76
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-120-377-76

  Query Match      87.6%;   Score 539;   DB 14;   Length 119;
  Best Local Similarity   88.2%;
  Matches  105;   Conservative  1;   Mismatches  13;   Indels  0;   Gaps  0;

Qy       1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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RESULT 9

US-10-980-815-76

Sequence 76, Application US/10980815

; Publication No. US20050059117A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P8
; CURRENT APPLICATION NUMBER: US/10/980,815
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/10/120,377
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,391
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/317,600
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 76
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-815-76

Query Match   87.6%; Score 539; DB 18; Length 119;
Best Local Similarity   88.2%; Pred. No. 5.6e-43;
Matches 105; Conservative   1; Mismatches 13; Indels   0; Gaps   0;

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Qy      1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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Db      1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVALIWYDGSNKYY 60

Qy     61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
          |||||||||||||||||||||||||| ||||||||||:   :    || |||||||||
Db     61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGCFDYWGQGTLVTVSS 119
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RESULT 10

US-10-992-196-76

Sequence 76, Application US/10992196

; Publication No. US20050192429A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P8P1
; CURRENT APPLICATION NUMBER: US/10/992,196
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: 60/523,661
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/283,391
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/317,600
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 10/120,377
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 76
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-196-76

Query Match   87.6%; Score 539; DB 17; Length 119;
Best Local Similarity   88.2%; Pred. No. 5.6e-43;
Matches 105; Conservative   1; Mismatches 13; Indels   0; Gaps   0;

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Qy      1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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Db      1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVALIWYDGSNKYY 60

Qy     61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
          |||||||||||||||||||||||||| ||||||||||:   :    || |||||||||
Db     61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGCFDYWGQGTLVTVSS 119
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RESULT 11

US-10-935-290-100

Sequence 100, Application US/10935290

; Publication No. US20050069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
; FILE REFERENCE: PF584P1
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 100
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv protein GMBC683
US-10-935-290-100

Query Match   87.6%; Score 538.5; DB 17; Length 241;
Best Local Similarity   88.2%; Pred. No. 1.3e-42;
Matches 105; Conservative   2; Mismatches 11; Indels   1; Gaps   1;

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Qy      1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
          |||||||||| :||||||||||||||||||||||||||||||||||||||||||| ||||
Db      1 QVQLVESGGGLVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy     61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGGCFDYWGQGTLVTVSS 119
          ||||||||||||||||||||||||||||||||||||||:  :     ||||||||||||
Db     61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGRAAAG-TLDYWGQGTLVTVSS 118
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RESULT 12

US-09-791-153A-63

Sequence 63, Application US/09791153A

; Publication No. US20030109978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 63
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-63

Query Match   87.5%; Score 538; DB 10; Length 113;
Best Local Similarity   89.1%; Pred. No. 6.6e-43;
Matches 106; Conservative   0; Mismatches   7; Indels   6; Gaps   1;

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Qy      1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
          :|||||||||| :|||||||||||||||||| ||||||||||||||||||||||| ||||
Db      1 EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy     61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
          |||||||||||||||||||||||||| ||||||||||:  :    ||| |||||||||
Db     61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGGCFDYWGQGTLVTVSS 118
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RESULT 14
US-10-727-155-92
Sequence 92, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenko
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: FACTOR AND USES THEREOF
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 92
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-92

Query Match   87.3%; Score 537; DB 17; Length 121;
Best Local Similarity   86.8%;
Matches 105; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

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Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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Db    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVSS 118
        |||||||||||||||||||||||||| |:||||||||:                       
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARESDYGGNPYFDYWGQGTLVTVSS 120
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RESULT 13
US-11-021-715-57
Sequence 57, Application US/11021715
Publication No. US20050208596A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: 053893-5050
CURRENT APPLICATION NUMBER: US/11/021,715
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: PCT/US03/21304
PRIOR FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/394,352
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: 60/411,694
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin version 3.2
SEQ ID NO 57
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-11-021-715-57

Query Match   87.3%; Score 537; DB 20; Length 117;
Best Local Similarity   88.2%; Pred. No. 8.5e-43;
Matches 105; Conservative 1; Mismatches 11; Indels 2; Gaps 1;

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Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
        ||||||||||||||||||||||||||||||| ||||||||||||||||| |||||| |||
Db    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
        ||||||||||||||||||||||||||:|||||||||:                       
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK------YFDYWGQGTLVTVSS 113
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RESULT 15
US-10-938-353-110
Sequence 110, Application US/10938353
Publication No. US20050059113A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: DEVALARAJA, MADHAV NARASIMHA
APPLICANT: FOLTZ, IAN
APPLICANT: HAAK-FRENDSCHO, MARY
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: LOW, JOSEPH EDWIN
APPLICANT: MOBLEY, JAMES LESLIE
TITLE OF INVENTION: ANTIBODIES TO M-CSF
FILE REFERENCE: ABX-PF4
CURRENT APPLICATION NUMBER: US/10/938,353
CURRENT FILING DATE: 2004-09-09
PRIOR APPLICATION NUMBER: 60/502,163
PRIOR FILING DATE: 2003-09-10
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 110
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-10-938-353-110

Query Match   87.1%; Score 535.5; DB 17; Length 117;
Best Local Similarity   88.2%; Pred. No. 1.2e-42;
Matches 105; Conservative 2; Mismatches 9; Indels 3; Gaps 1;

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Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
        ||||||||||||||||||||||||||||||| ||||||||||||||||| | |||| |||
Db    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
        ||||||||||||||||||||||||||:|||||||||:                       
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGYS---YFDYWGQGTLVTVSS 116
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Search completed: October 13, 2005, 03:02:47
Job time : 116.425 secs

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Title: OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: October 13, 2005, 02:37:04 ; Search time 19.4077 Seconds
(without alignments)
457.717 Million cell updates/sec

Title: US-10-010-729A-7
Perfect score: 615
Sequence: 1 QVQLVESGGGVVQPGRSLRL..........VTGSPTLDYWGQGTLVTVSS 119

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Searched: 513545 seqs, 74649064 residues

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Issued_Patents AA:*
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	542.5	88.2	248	4	US-09-315-926A-80	Sequence 80, Appl
2	531	86.3	119	1	US-08-331-398A-46	Sequence 46, Appl
3	531	86.3	119	1	US-08-331-397B-46	Sequence 46, Appl
4	531	86.3	119	2	US-08-331-398A-46	Sequence 46, Appl
5	531	86.3	119	3	US-08-759-804A-46	Sequence 46, Appl
6	531	86.3	119	3	US-09-227-693-46	Sequence 46, Appli
7	525.5	85.4	463	4	US-09-472-087-1	Sequence 1, Appli
8	525.5	85.4	463	4	US-09-472-087-63	Sequence 63, Appli
9	525	85.4	120	1	US-07-942-245-35	Sequence 35, Appl
10	525	85.4	463	4	US-09-472-087-64	Sequence 64, Appli
11	521	84.7	225	4	US-09-456-090A-92	Sequence 92, Appl
12	521	84.7	225	4	US-09-453-234-60	Sequence 60, Appl
13	521	84.7	225	4	US-09-453-234-92	Sequence 92, Appl
14	520	84.6	225	4	US-09-456-090A-108	Sequence 108, Appl
15	520	84.6	225	4	US-09-453-234-108	Sequence 108, App
16	520	84.6	451	4	US-09-472-087-70	Sequence 70, Appli
17	517	84.1	464	4	US-09-472-087-2	Sequence 2, Appli
18	517	84.1	464	4	US-09-472-087-66	Sequence 66, Appli
19	515.5	83.8	463	4	US-09-472-087-4	Sequence 4, Appli
20	515.5	83.8	463	4	US-09-472-087-68	Sequence 68, Appl
21	515	83.7	225	4	US-09-456-090A-102	Sequence 102, App
22	515	83.7	225	4	US-09-453-234-102	Sequence 102, App
23	515	83.7	225	4	US-09-453-234-106	Sequence 106, App
24	515	83.7	123	4	US-09-560-198A-2	Sequence 2, Appli
25	513	83.4	225	4	US-09-456-090A-56	Sequence 56, Appl
26	513	83.4	225	4	US-09-456-090A-68	Sequence 68, Appl
27	513	83.4	225	4	US-09-456-090A-68	Sequence 68, App
28	513	83.4	225	4	US-09-456-090A-110	Sequence 110, Appl
29	513	83.4	225	4	US-09-453-234-56	Sequence 56, Appl
30	513	83.4	225	4	US-09-453-234-68	Sequence 68, Appl
31	513	83.4	225	4	US-09-453-234-110	Sequence 110, App
32	513	83.1	115	3	US-09-726-219A-167	Sequence 167, App
33	511	83.1	115	3	US-09-560-198A-10	Sequence 10, Appl
34	510	82.9	123	4	US-09-424-840B-16	Sequence 16, Appli
35	509	82.8	117	3	US-09-025-769B-24	Sequence 24, Appl
36	509	82.8	117	4	US-09-490-070A-24	Sequence 24, Appl
37	507	82.4	117	4	US-09-490-153-24	Sequence 24, Appl
38	507	82.4	225	4	US-09-240-274-24	Sequence 24, Appl
39	507	82.4	225	3	US-09-456-090A-94	Sequence 94, Appl
40	507	82.4	225	4	US-09-240-274-94	Sequence 94, Appl
41	506	82.2	125	3	US-09-453-234-94	Sequence 94, Appl
42	505.5	82.2	124	4	US-09-424-840B-16	Sequence 16, Appl
43	505	82.1	119	4	US-09-648-067A-15	Sequence 15, Appli
44	502.5	81.7	310	4	US-09-079-029-11	Sequence 11, Appl
45	502	81.6	116	1	US-08-211-202-141	Sequence 141, App

ALIGNMENTS

RESULT 1
US-09-315-926A-80
Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmuth
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlijden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80

Query Match 88.2%; Score 542.5; DB 4; Length 248;
Best Local Similarity 87.5%; Pred. No. 1.9e-44;
Matches 105; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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Db 23 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLTPXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
      ||||||||||||||||||||||||| : ||||||||||: || ||||||||||||||
Db 83 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 142

RESULT 2
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark

; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
;   and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew
;   STREET: One Market Plaza, Steuart Street Plaza
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105-1492
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/331,398A
;   FILING DATE: 28-OCT-1994
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/767,331
;   FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/596,289
;   FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hunter, Tom
;   REGISTRATION NUMBER: 38,498
;   REFERENCE/DOCKET NUMBER: 015280-12611OUS
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 543-9600
;   TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..119
;   OTHER INFORMATION: /note= "Human fetal immunoglobulin
;   Variable Heavy chain (V-H)"
US-08-331-398A-46

Query Match   86.3%; Score 531; DB 1; Length 119;
Best Local Similarity   86.6%; Pred. No. 1.1e-43;
Matches 103; Conservative   3; Mismatches 13; Indels 0; Gaps 0;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||| ||| ||.|||||||||||||.|||||.|||
Db   1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| |.|||||||||. ||.||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119

RESULT 3
US-08-331-397B-46
; Sequence 46, Application US/0831397B
; Patent No. 5981726
; GENERAL INFORMATION:
;   APPLICANT: Pastan, Ira
;   APPLICANT: Benhar, Itai
;   TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
;   TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
;   TITLE OF INVENTION: Thereof
;   NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew
;   STREET: One Market Plaza, Steuart Street Plaza
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105-1492
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/331,397B
;   FILING DATE: 28-OCT-1994
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/767,331
;   FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 07/596,289
;   FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hunter, Tom
;   REGISTRATION NUMBER: 38,498
;   REFERENCE/DOCKET NUMBER: 015280-12612OUS
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 543-9600
;   TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 119 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..119
;   OTHER INFORMATION: /note= "Human fetal immunoglobulin
;   Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match   86.3%; Score 531; DB 2; Length 119;
Best Local Similarity   86.6%; Pred. No. 1.1e-43;
Matches 103; Conservative   3; Mismatches 13; Indels 0; Gaps 0;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||| ||| ||.|||||||||||||.|||||.|||
Db   1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| |.|||||||||:   :||:|||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119

RESULT 4
US-08-759-804A-46
; Sequence 46, Application US/0875980A
; Patent No. 5990296
; GENERAL INFORMATION:
;   APPLICANT: Pastan, Ira
;   APPLICANT: Willingham, Mark
;   APPLICANT: Fitzgerald, David J.
;   APPLICANT: Brinkmann, Ulrich
;   APPLICANT: Pai, Lee
;   TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
;   TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
;   NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco

```
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-12614OUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
US-08-759-804A-46                 56P1'Cl Variable Heavy chain (V-H)"

Query Match             86.3%;  Score 531;  DB 2;  Length 119;
Best Local Similarity   86.6%;  Pred. No. 1.1e-43;
Matches 103;  Conservative   3;  Mismatches  13;  Indels   0;  Gaps   0;

Qy     1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db     1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy    61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
           |||||||||||||||||||||||||| ||||||||||||:
Db    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119
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RESULT 5
US-09-227-693-46
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; Sequence 46, Application US/0922 7693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
```

```
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
TELEFAX: (415) 543-9600
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
US-09-227-693-46                       56P1'Cl VH region"

Query Match             86.3%;  Score 531;  DB 3;  Length 119;
Best Local Similarity   86.6%;  Pred. No. 1.1e-43;
Matches 103;  Conservative   3;  Mismatches  13;  Indels   0;  Gaps   0;

Qy     1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db     1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy    61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
           |||||||||||||||||||||||||| ||||||||||||:
Db    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119
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RESULT 6
US-09-472-087-1
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; Sequence 1, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-472-087-1

Qy Query Match 85.4%; Score 525.5; DB 4; Length 463;
 Best Local Similarity 86.6%; Pred. No. 1.6e-42;
 Matches 103; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
   |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 20 QVQLVESGGGVVQPGRSLRLSCVASGFTFSSHGMHWVRQAPGKGLEWVAVIWYDGRNKYY 79

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
   ||||||||||||||||||| |||||||:|:|||||||||||| ||| ||||||||||||
Db 80 ADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCARGGHFGP-FDYWGQGTLVTVSS 137

RESULT 7
US-09-472-087-63
; Sequence 63, Application US/09472087
; Patent No. 6682736

GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 63
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-472-087-63

Qy Query Match 85.4%; Score 525.5; DB 4; Length 463;
 Best Local Similarity 86.6%; Pred. No. 1.6e-42;
 Matches 103; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
   |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 20 QVQLVESGGGVVQPGRSLRLSCVASGFTFSSHGMHWVRQAPGKGLEWVAVIWYDGRNKYY 79

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
   ||||||||||||||||||| |||||||:|:|||||||||||| ||| ||||||||||||
Db 80 ADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCARGGHFGP-FDYWGQGTLVTVSS 137

RESULT 8
US-09-472-087-64
; Sequence 64, Application US/09472087
; Patent No. 6682736

GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 64
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-472-087-64

Qy Query Match 85.4%; Score 525.5; DB 4; Length 463;
 Best Local Similarity 86.6%; Pred. No. 1.6e-42;
 Matches 103; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
   |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 20 QVQLVESGGGVVQPGRSLRLSCVASGFTFSSHGMHWVRQAPGKGLEWVAVIWYDGRNKYY 79

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
   ||||||||||||||||||| |||||||:|:|||||||||||| ||| ||||||||||||
Db 80 ADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCARGGHFGP-FDYWGQGTLVTVSS 137

RESULT 9
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641

GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pensylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103

INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-07-942-245-35

Qy Query Match 85.4%; Score 525; DB 1; Length 120;
 Best Local Similarity 86.7%; Pred. No. 4.2e-43;
 Matches 104; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
   |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 1 QVQLVESGGGVVQPGRSLRLSCVASGFTFSSYAHHWVRQAPGKGLEWVAVISYDGSNKYY 60

```
Qy    61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT--GSPTLDYWGQGTLVTVS 118
         ||||||||||||||||||||||||||||||||||||||:||    ||||||||||||||||||
Db    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGWALFDYWGQGTLVTVSS 120
```

RESULT 10
US-09-456-090A-60
; Sequence 60, Application US/0945609A
; Patent No. 668209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-0002000US
; CURRENT APPLICATION NUMBER: 020015-0002000US
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 60
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-5H
US-09-456-090A-60

Query Match   84.7%; Score 521; DB 4; Length 225;
Best Local Similarity   85.7%; Pred. No. 2e-42;
Matches   102; Conservative   2; Mismatches 13; Indels   2; Gaps   1;

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Qy     1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         ||||||||||||||||||||||||||||||||||||||:|||    |:||||||||||||||| ||
Db     1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVTLIYTDGDNKYY 60

Qy    61 ADSVKGRFTISRDNSKNTLYLQMNSLTFAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
         ||||||||||||||||||||||||||||||||||||||||:||    ||||||||||||||||||
Db    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DGIGYFDYWGQGTLVTVSS 117
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RESULT 11
US-09-456-090A-92
; Sequence 92, Application US/0945609A
; Patent No. 668209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-0002000US
; CURRENT APPLICATION NUMBER: 020015-0002000US
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 92
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-11H
US-09-456-090A-92

Query Match   84.7%; Score 521; DB 4; Length 225;
Best Local Similarity   85.7%; Pred. No. 2e-42;
Matches   102; Conservative   2; Mismatches 13; Indels   2; Gaps   1;

```
Qy     1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         ||||||||||||||||||||||||||||||||||||||:|||    |:||||||||||||||||
Db     1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVTLIYTDGDNKYY 60

Qy    61 ADSVKGRFTISRDNSKNTLYLQMNSLTFAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
         |||||||||||||||||||||||||||||||||||||||:||    ||||||||||||||||||
Db    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DGIGYFDYWGQGTLVTVSS 117
```

RESULT 12
US-09-453-234-60
; Sequence 60, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-0001100US
; CURRENT APPLICATION NUMBER: 020015-0001100US
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 60
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-5H
US-09-453-234-60

Query Match   84.7%; Score 521; DB 4; Length 225;
Best Local Similarity   85.7%; Pred. No. 2e-42;
Matches   102; Conservative   2; Mismatches 13; Indels   2; Gaps   1;

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Qy     1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         ||||||||||||||||||||||||||||||||||||||:|||    |:||||||||||||||||
Db     1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVTLIYTDGDNKYY 60

Qy    61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
         ||||||||||||||||||||||||||||||||||||||:||    ||||||||||||||||||
Db    61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DGIGYFDYWGQGTLVTVSS 117
```

RESULT 13
US-09-453-234-92
; Sequence 92, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-0001100US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 92
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-11H
US-09-453-234-92

Query Match   84.7%; Score 521; DB 4; Length 225;
Best Local Similarity   85.7%; Pred. No. 2e-42;
Matches   102; Conservative   2; Mismatches 13; Indels   2; Gaps   1;

```
Qy     1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        1  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVTLITYDYNKYY  60
                                                                       
Qy       61  ADSVKGRFTISRDNSKNTLYLQMNSLITAXDTAVYYCAKGVTGSSPTLDYWGQGTLVTVSS  119
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61  ADSVKGRFTISRDNSKNTLIYLQMNSLRAEDTAVYYCAR--DGIGYPDYWGQGTLVTVSS  117
```

RESULT 14
US-09-456-090A-108
; Sequence 108, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-00020US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 108
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34H
US-09-456-090A-108

Query Match   84.6%; Score 520; DB 4; Length 225;
Best Local Similarity 85.7%; Pred. No. 2.5e-42;
Matches 102; Conservative 2; Mismatches 13; Indels 2; Gaps 1;

```
Qy        1  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY  60
             |||||||||||||||||||||||||||||||| ||||||||||||||| :||| |||
Db        1  QVQLVESGGGVVQPGRSLRLSCAASGFTFSYYGIHHWRQVPGKGLEWVVLISYDGSNKYY  60

Qy       61  ADSVKGRFTISRDNSKNTLIYLQMNSLITAXDTAVYYCAKGVTGSSPTLDYWGQGTLVTVSS  119
             ||||||||||||||||||||||||||||  :|||||||||  ||||||||||||||||
Db       61  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWIG--YFDYWGQGTLVTVSS  117
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RESULT 15
US-09-453-234-108
; Sequence 108, Application US/0945234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-00010US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 108
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34H
US-09-453-234-108

Query Match   84.6%; Score 520; DB 4; Length 225;
Best Local Similarity 85.7%; Pred. No. 2.5e-42;
Matches 102; Conservative 2; Mismatches 13; Indels 2; Gaps 1;

```
Qy        1  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY  60
```

Search completed: October 13, 2005, 02:45:19
Job time : 20.4077 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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```
                              GenCore version 5.1.6
                              Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:           October 13, 2005, 02:45:26 ; Search time 118.489 Seconds
                              (without alignments)
                              514.286 Million cell updates/sec

Title:            US-10-010-729A-7
Perfect score:    615
Sequence:         1 QVQLVESGGGVVQPGRSLRL.........VTGSPTLDYWGQGTLVTVSS 119

Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched:         1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:   1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Uniprot_03:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

* Pred. No. is the number of results predicted by chance to have a
  score greater than or equal to the score of the result being printed,
  and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	537.5	87.4	613	2	Q8WUK1	homo sapien
2	525	85.4	116	2	Q9U193	homo sapien
3	523	85.0	113	2	Q9U190	homo sapien
4	513	83.4	240	2	Q65ZC9	homo sapien
5	490.5	79.8	122	2	Q9U184	homo sapien
6	489.5	79.6	122	1	HV3G_HUMAN	homo sapien
7	482.5	78.5	147	2	P01768	homo sapien
8	482	78.4	121	1	Q9Y509	homo sapien
9	482	78.4	121	2	P01771	homo sapien
10	474	77.1	121	1	HV3J_HUMAN	homo sapien
11	471	76.6	493	2	Q9U171	homo sapien
12	468	76.1	597	2	Q6GMX2	homo sapien
13	467.5	76.0	122	1	HV3H_HUMAN	homo sapien
14	467	75.9	478	2	P01769	homo sapien
15	464.5	75.5	544	2	Q6p181	homo sapien
16	464	75.4	119	2	Q6p295	homo sapien
17	462	75.1	470	2	HV3I_HUMAN	homo sapien
18	460.5	74.9	119	2	P01770	homo sapien
19	460	74.8	464	2	Q6pJa4	homo sapien
20	459.5	74.7	573	2	Q8WU38	homo sapien
21	458.5	74.6	116	1	HV3T_HUMAN	homo sapien
22	458	74.5	493	2	P01781	homo sapien
23	456.5	74.2	118	2	Q8NCL6	homo sapien
24	453	73.7	472	2	Q9U191	homo sapien
25	452.5	73.6	126	1	HV3K_HUMAN	homo sapien
26	452	73.5	466	2	Q6N089	homo sapien
27	450	73.2	519	2	Q6N092	homo sapien
28	449	73.0	119	1	HV3L_HUMAN	homo sapien
29	446.5	72.6	479	2	Q6MZV6	homo sapien
30	443	72.1	473	2	Q6MZV7	homo sapien
31	442.5	72.0	112	2	Q9HCC1	homo sapien
32	442	71.9	482	2	Q7Z351	homo sapien
33	441.5	71.8	114	1	HV3B_HUMAN	homo sapien
34	438.5	71.3	136	1	HV16_MOUSE	mus musculu
35	436	70.9	499	2	Q8N5K4	homo sapien
36	435.5	70.8	465	2	Q6PC4	homo sapien
37	434.5	70.7	487	2	Q99KA4	mus musculu
38	433	70.4	480	2	Q6N094	homo sapien
39	430.5	70.0	473	2	Q91205	homo sapien
40	429	69.8	119	2	Q6MZX9	homo sapien
41	426	69.3	485	2	Q6PDB8	mus musculu
42	425.5	69.2	483	2	Q6PDB8	mus musculu
43	420.5	68.4	494	2	Q96K68	homo sapien
44	419.5	68.2	119	1	HV3M_HUMAN	homo sapien
45	419.5	68.2	475	2	Q6MZQ6	homo sapien

ALIGNMENTS

RESULT 1
Q8WUK1

```
ID   Q8WUK1      PRELIMINARY;      PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020240; AAH20240.1; -.
DR   PIR; F36005; F36005.
DR   PIR; G36005; G36005.
DR   PIR; PH1642; PH1642.
DR   PIR; PH1643; PH1643.
DR   PIR; PH1645; PH1645.
DR   PIR; PH1646; PH1646.
DR   PIR; PH1645; PH1645.
DR   PIR; PL0098; PL0098.
DR   PIR; PL0120; PL0120.
DR   PIR; S15590; S15590.
DR   PIR; S31116; S31116.
DR   PIR; S31119; S31119.
DR   PIR; S70442; S70442.
```

```
DR   HSSP; P01861; 1ADQ.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   613 AA;  67295 MW;  60C7F59506571E3315 CRC64;

Query Match             87.4%;  Score 537.5;  DB 2;  Length 613;
Best Local Similarity   88.3%;  Pred. No. 1.5e-49;
Matches 106; Conservative  2; Mismatches  11; Indels  1; Gaps  1;

Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
          ||||||||||||||||||||||||||||||||  |||||||||||||  ||||||||
Db   20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT-GSPTLDYWGQGTLVTVSS 119
          |||||||||||||||||||||||| ||||||||||||    |||||||||||||||
Db   80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEBDTAVYYCAKDWSEGVEVTFDIWGQGTMVTVSS 139
```

RESULT 2
```
ID   Q9UL93             PRELIMINARY;       PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; AAD56257.1; -.
DR   PIR; PH1644; PH1644.
DR   PIR; PL0120; PL0120.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
NON_TER        1           1
NON_TER      116         116
FT   NON_TER       1       1
SQ   SEQUENCE   116 AA;  12434 MW;  0DA03481540DD6061 CRC64;
```

Query Match   85.4%; Score 525; DB 2; Length 116;
Best Local Similarity   88.1%; Pred. No. 5e-49;
Matches 104; Conservative 1; Mismatches 11; Indels 2; Gaps 1;

```
Qy    2 VQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYYA 61
          |||||||||||||||||||||||||||||| |||||||||||||||  |||||||||
Db    1 VQLVESGGGVVQPGRSLRLSCAASGFTFSSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 60

Qy   62 DSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   61 DSVKGRFTISRDNSKNTLYLQMNSLRAEBDTAMYYCAGG--GGLGLGYWGQGTLVTVSS 116
```

RESULT 3
```
ID   Q9UL90             PRELIMINARY;       PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035024; AAD56260.1; -.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
NON_TER   1   1
NON_TER   113   113
FT   NON_TER   1   1
SQ   SEQUENCE   113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match   85.0%; Score 523; DB 2; Length 113;
Best Local Similarity   86.6%; Pred. No. 8.1e-49;
Matches 103; Conservative 2; Mismatches 8; Indels 6; Gaps 1;

```
Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
          ||||||||||||||||||||||||||||||||  |||||||||||||  ||||||||
Db    1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
          |||||||||||||||||||||||||          ||||||||||||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEBDTAVYYCAK-------DLNYWGQGTLVTVSS 113
```

RESULT 4
```
ID   Q65ZC9             PRELIMINARY;       PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
NON_TER        1           1
NON_TER      240         240
FT   NON_TER       1       1
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;
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Query Match   83.4%; Score 513; DB 2; Length 240;
Best Local Similarity   84.9%; Pred. No. 2.3e-47;
Matches 101; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

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Qy           1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
               |||:||||||||||:||||||||||||||||||||||||||||||||||||||||:|||||
Qy           1 QVQVQSGGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy          61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
               |||||||||||||||||||||||||:|||||||||||||||||||||||||||||:|||
Db          61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DWGDSLDPWGKGTLVTVSS 117
```

RESULT 5
ID   Q9UL84
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   NON_TER 1 1
DR   SEQUENCE 122 AA; 13579 MW; 36054D413665A5B8 CRC64;

PRELIMINARY;   PRT;   122 AA.

Query Match   79.8%; Score 490.5; DB 2; Length 122;
Best Local Similarity   80.3%; Pred. No. 3e-45;
Matches 98; Conservative 4; Mismatches 17; Indels 3; Gaps 1;

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Qy           1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
               :||||||||||||||||:|||||||||||||||||||||||||||||||||||||:|||||
Db           1 EVQLVESGGGVVQPGRSLRLSCAASRFTFSNYGMHWVRQAPGKGLEWVAAISNDGSNKFY 60

Qy          61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTG---SPTLDYWGQGTLVTV 117
               |||||||||||||||||||||||||||:|||||||||||:||   ||||||||||||||||
Db          61 ADSVKGRFTIFRDNSKNMDLQMNSLRAEDTAVYYCARDERGRLVGTYFDYWGQGTLVTV 120
```

```
Qy         118 SS 119
               ||
Db         121 SS 122
```

RESULT 6
ID   HV3G_HUMAN   STANDARD;   PRT;   122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;

```
Qy           1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
               ||||||||||:|||||||||||||||||||||||||||||||||||||||:||||||||||
Db           1 QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY 60

Qy          61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG---VTGS-PTLDYWGQGTLVTV 117
               |||||||||||||:||||||||||||||:||||||||||   |||| ||||||||||||||
Db          61 ADSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQGTLVTV 120
```

```
Qy         118 SS 119
               ||
Db         121 SS 122
```

RESULT 7
ID   Q9Y509
AC   Q9Y509;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH3 protein (Fragment).
GN   Name=VH3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96071149; PubMed=7475288;
RA   Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA   Lichtenstein A.K., Berenson J.R.;
RT   "A CD10-positive subset of malignant cells is identified in multiple
RT   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL   Leukemia 9:1948-1953(1995).
DR   EMBL; S80860; AAD14339.1; -.
DR   HSSP; P01842; 1AOK.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   NON_TER 147 147
DR   SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

PRELIMINARY;   PRT;   147 AA.

Query Match   79.6%; Score 489.5; DB 1; Length 122;
Best Local Similarity   77.0%; Pred. No. 3.8e-45;
Matches 94; Conservative 11; Mismatches 14; Indels 3; Gaps 2;

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Qy           1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
               |:||||||||||:||||||||||||||||||:|||||||||||||||||||:|||||||||
Db           1 QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY 60

Qy          61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG---VTGS-PTLDYWGQGTLVTV 117
               |||||||||||||:||||||||||||||:||||||||||   |||| ||||||||||||||
Db          61 ADSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQGTLVTV 120
```

```
Qy         118 SS 119
               ||
Db         121 SS 122
```

RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!-   MISCELLANEOUS: This mu chain was isolated from the plasma of a
         patient with macroglobulinemia.
-!-   SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR;   A02051; M3HUM.
HSSP;   P01772; 2FB4.
GO;   GO:0005576; C:extracellular; NAS.
GO;   GO:0003823; F:antigen binding; NAS.
GO;   GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam;   PF00047; ig; 1.
SMART;   SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
DOMAIN   1 112   Ig-like.
MOD_RES 1 1   Pyrrolidone carboxylic acid.
NON_TER 112 112
SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Qy 112 GTLVTVSS 119
       ||||||||
Db 119 GTLVTVSS 126

RESULT 8

ID   HV3J_HUMAN   STANDARD;   PRT;   121 AA.
AC   P01771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region HIL.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79124695; PubMed=420800;
RA   Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT   "Amino acid sequence of the VH region of human myeloma
RT   cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 18:553-560(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC   protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02054; GIHUHL.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN   1   112   Ig-like.
FT   MOD_RES   1   1   Pyrrolidone carboxylic acid.
FT   NON_TER   121   121
SQ   SEQUENCE   121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match   78.4%; Score 482; DB 1; Length 121;
Best Local Similarity   76.0%; Pred. No. 2.5e-44;
Matches   92; Conservative   11; Mismatches   16; Indels   2; Gaps   1;

Qy   1 QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWNGSRTTY 60
         ||:|:|||||||||||||||||:|||||||||:||||||||||||||||:::||:||||
Db   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVS 118
         |||||||||||||||| ||||||||||:||:||||||| |:||||||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCARDPDILTAFSFDYWGQGVLVTVS 120

RESULT 9

ID   Q9UL71   PRELIMINARY;   PRT;   121 AA.
AC   Q9UL71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035043; AAD56279.1; -.
DR   HSSP; P01852; INFD.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER   1   1
FT   NON_TER   121   121
SQ   SEQUENCE   121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match   77.1%; Score 474; DB 2; Length 121;
Best Local Similarity   77.7%; Pred. No. 1.8e-43;
Matches   94; Conservative   5; Mismatches   20; Indels   2; Gaps   1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         ||||||||||||||||||||||||||||:::::||:||||||||||||||:::||:||||
Db   1 EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG--VTGSPTLDYWGQGTLVTVS 118
         ||||||||||||||||| ||||||||:|:||||||||| |:||||||||||||||||
Db   61 ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDRPDIWGQGTMVTVS 120

Qy 119 S 119
         |
Db 121 S 121

RESULT 10

ID   Q6GMX2   PRELIMINARY;   PRT;   493 AA.
AC   Q6GMX2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RESULT 11

ID   Q96BB9   PRELIMINARY;   PRT;   597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Qy   1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKXY 60
        ||||||||| ||||||||||||||||||||||||||||||||||||:||| |||||||||
Db   20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLVWVSRINSDGSSTSY 79

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCXAXGVTGSP--TLDYWGQGTLVTVS 118
        ||||||||||||:|| |||||||||||| ||||||||| ||||| |||||||||||||
Db   80 ADSVKGRFTISRDNAKNTLYLQMNSLRGEDAAVYYCARGFVSLPRSTLDIWGQGTMVTVS 139

Qy 119 S 119
        |
Db 140 S 140

Query Match   76.6%; Score 471; DB 2; Length 493;
Best Local Similarity   76.9%; Pred. No. 1.9e-42;
Matches   93; Conservative 7; Mismatches 19; Indels 2; Gaps 1;

RESULT 12

ID   HV3H_HUMAN   STANDARD;   PRT;   122 AA.
AC   P01769;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region GA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=74175307; PubMed=4208843;
RA   Florent G., Lehman D., Putnam F.W.;
RT   "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL   Biochemistry 13:2482-2498(1974).
CC   -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC   macroglobulin.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02052; M3HUGA.
DR   HSSP; P01772; 2F8A.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.

Qy   1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKXY 60
        ||||||||| ||||||||||||||||||||||||||||||||||||:||| |||||||||
Db   20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVSAISGSGGSTYY 79

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCXAX------GVTGSPTL-DYWGQGTL 114
        ||||||||||:|| |||||||||||| |||||||| ||| |:||| |||||||
Db   80 ADSVKGRFTISRDNSRDTLYLQMNSLRABDTAVYYCAKDPRGYSASGNTREDVWGQGTL 139

Qy 115 VTVSS 119
        |||||
Db 140 VTVSS 144

Query Match   76.1%; Score 468; DB 2; Length 597;
Best Local Similarity   75.2%; Pred. No. 5e-42;
Matches   94; Conservative 10; Mismatches 15; Indels 6; Gaps 2;

SQ   SEQUENCE   597 AA; 65039 MW; 4FCA3AD8ECB263D9 CRC64;

Left column (RESULT 11 bibliographic continued):

RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA   Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073771; AAH73771.1; -.
DR   InterPro; IPR000599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; Ig; 3.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   493 AA; 55B99305B2B6203 CRC64;
KW   Hypothetical protein.

Left column (RESULT 12 bibliographic):

RA   Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA   Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
DR   PIR; S05271; S05271.
DR   PIR; S24260; S24260.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS08835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.

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DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Pyrrolidone carboxylic acid.
KW   Direct protein sequencing; Immunoglobulin V region;
FT   DOMAIN     1  112
FT   MOD_RES    1    1       Pyrrolidone carboxylic acid.
FT   NON_TER    1    1
FT   SEQUENCE  122 AA; 13166 MW; 74B5B6959B84100A CRC64;
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Query Match          76.0%; Score 467.5; DB 1; Length 122;
Best Local Similarity 68.0%; Pred. No. 9.3e-43;
Matches  85; Conservative  20; Mismatches  11; Indels   9; Gaps   2;

Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
        |||||| ||| | ||||||||||||||| |   |||||||||||||   | ||| |  || 
Db    1 QVQLVZSGGGAVZPGRSLRLSCAASGFSTYAMHWVRQAPGKGLZMLSVISYBGBBZYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK------GVTGSPFLDYWGQGTL 114
        | ||||||||||  ||  | |::|||||   ||||||:      | |:||||||:|||
Db   61 AASVKGRFTISRBBSKBTMYLEMNSLRABNTAVYYCARSGIALGSVAGT--DYWGZGTL 117

Qy  115 VTVSS 119
        ||:||
Db  118 VTISS 122
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RESULT 13
Q6PI81
ID   Q6PI81           PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   HSSP; P01861; 1ADQ.
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DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE  478 AA; 52666 MW; 17BED38D91797OD6 CRC64;
```

```
Query Match          75.9%; Score 467; DB 2; Length 478;
Best Local Similarity 72.1%; Pred. No. 5e-42;
Matches  93; Conservative   8; Mismatches  18; Indels  10; Gaps   1;

Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
        |||||||||||:||| ||||||||||||||| :|||||||||||||||| :| | ||||
Db   20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYXMHWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT------LDYWG 110
        .|||||||||||||:||:|||||||||:| ||||||||:|:|| |||     |||||
Db   80 VDSVKGRFTISRDNAKNSLYLQMNSLRABDTAVYYCAREFESTMTTVNADYYFYMDVWG 139
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RESULT 14
Q6PJ95
ID   Q6PJ95           PRELIMINARY;      PRT;   544 AA.
AC   Q6PJ95;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019046; AAH19046.1; -.
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DR   HSSP; P01861; 1AD0.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00408; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   544 AA;  60102 MW;  1895814B2297C668 CRC64;

Query Match
Best Local Similarity   75.5%;   Score 464.5; DB 2; Length 544;
Matches   96;  Conservative   3;  Mismatches  20;  Indels   7;  Gaps   2;

Qy    1  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY   60
         |||||||||||||||:|||||||||||:|:||||:|||||||||||||||:::|||||:|
Db   20  QAQLVESGGGVVQPGSSLRLSCAASGFRFSNYGMHWVRQAPGKGLEWVAVFSYDESDKYY   79

Qy   61  ADSVKGRFTISRDNSKNTLYLQMNSLITAXDTAVYYCAKG----VTGS---PTLDYWGQGT  113
         ||:|||||||||||:||||||:|||||||||||||||||          ::|||||||||
Db   80  AASVKGRFTISRDNSKNTLSLQMNSLRVEDTAVYYCAKDQKPWYSNSWFLTNFDSWGRGT  139

Qy  114  LVTVSS  119
         ||||||
Db  140  LVTVSS  145
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RESULT 15
ID   HV31_HUMAN     STANDARD;     PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), III. The chymotryptic
RT   peptides of the H-chain, alignment of the tryptic peptides and
RT   discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A91668; GIHUNI.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig-v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN     1    112     Ig-like.
FT   MOD_RES    1      1     Pyrrolidone carboxylic acid.
FT   NON_TER  119    119
FT   DISULFID  22     96
SQ   SEQUENCE   119 AA;  13242 MW;  C96935A6E55B165B CRC64;

Query Match
Best Local Similarity   75.4%;   Score 464; DB 1; Length 119;
Matches   90;  Conservative  10;  Mismatches  19;  Indels   0;  Gaps   0;

Qy    1  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY   60
         |||||:|||||||||||||||||||||:||:|:||||||||||||||||::|||:|||||
Db    1  QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY  60

Qy   61  ADSVKGRFTISRDNSKNTLYLQMNSLITAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS  119
         ||||:||||||||:|||||||:|||||:|||||||||||:|:||||||||||:||||||
Db   61  ADSVNGRFTISRNDSKNTLYLNMNSLRPEDTAVYYCARIRDTAMFPAHWGQGTLVTVSS  119
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Search completed: October 13, 2005, 03:10:52
Job time : 120.489 secs

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: October 13, 2005, 02:57:16 ; Search time 24.515 Seconds
(without alignments)
467.052 Million cell updates/sec

Title: US-10-010-729A-7
Perfect score: 615
Sequence: 1 QVQLVESGGGVVQPGRSLRL.........VTGSPTLDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_79:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	536	87.2	121	2	S19666	Ig heavy chain V r
2	533.5	86.7	120	2	S31112	Ig heavy chain - h
3	533.5	86.7	122	2	S36278	Ig heavy chain V r
4	533	86.7	134	2	S31679	Ig heavy chain V-I
5	532	86.5	119	2	F36005	Ig heavy chain V r
6	531	86.3	132	2	S31603	Ig heavy chain V r
7	530.5	86.3	140	2	S70442	Ig heavy chain V r
8	529	86.0	121	2	G36005	Ig heavy chain pre
9	528.5	85.9	118	2	S31116	Ig heavy chain V r
10	527	85.7	130	2	S31601	Ig heavy chain - h
11	527	85.7	135	2	S31598	Ig heavy chain V r
12	524	85.2	111	2	PH1643	Ig heavy chain V r
13	522.5	85.0	114	2	S46390	Ig heavy chain V r
14	521	84.7	133	2	A49028	Ig heavy chain V-I
15	519.5	84.5	139	2	S31674	Ig heavy chain V r
16	516.5	84.0	122	2	E36005	Ig heavy chain - h
17	509.5	82.8	114	2	S46392	Ig heavy chain V r
18	509	82.8	130	2	PL0098	Ig heavy chain pre
19	508.5	82.7	137	2	S31701	Ig heavy chain V r
20	507.5	82.5	128	2	S48797	Ig heavy chain V r
21	507.5	82.5	151	2	A60943	Ig heavy chain V r
22	504	82.0	109	2	PH1644	Ig heavy chain V r
23	502.5	81.7	133	2	S31510	Ig heavy chain V r
24	496	80.7	123	2	S38493	Ig heavy chain - h
25	495.5	80.7	114	2	S46391	Ig heavy chain V r
26	495.5	80.6	114	2	S38490	Ig heavy chain - h
27	493	80.4	136	2	S31587	Ig heavy chain V r
28	493	80.2	109	2	PH1646	Ig heavy chain V r
29	492	80.0	140	2	S31686	Ig heavy chain V r
30	491	79.8	111	2	PH1645	Ig heavy chain V r
30	491	79.8	117	2	S78486	Ig heavy chain V r
31	490	79.7	119	2	S31107	Ig heavy chain - h
32	490	79.7	120	2	S36278	Ig heavy chain V r
33	489.5	79.6	122	1	M3HUAM	Ig heavy chain V-I
34	489.5	79.6	122	2	S69910	Ig heavy chain - h
35	488	79.3	119	2	S31108	Ig heavy chain - h
36	488	79.3	121	2	I55673	Ig V-D-J region (K
37	485.5	78.9	121	2	S31119	Ig heavy chain - h
38	485	78.9	113	2	S38490	Ig heavy chain - h
39	485	78.9	122	2	C36005	Ig variable region
40	482.5	78.5	147	2	I37780	Ig heavy chain V r
41	482	78.4	98	2	PL0116	Ig heavy chain - h
42	482	78.4	121	1	G1HUHL	Ig heavy chain - h
43	482	78.4	138	2	B56701	Ig heavy chain V r
44	481	78.2	138	2	S31666	Ig heavy chain V r
45	480.5	78.1	120	2	S44111	Ig heavy chain V-D

ALIGNMENTS

RESULT 1
S19666
Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
J. Mol. Biol. 222, 581-597, 1991
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter.
R;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19666
A;Molecule type: mRNA
A;Residues: 1-121 <MAR>
A;Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match          87.2%;  Score 536;  DB 2;  Length 121;
Best Local Similarity 87.0%;
Matches  107;  Conservative   2;  Mismatches   8;  Indels   6;  Gaps  2;

Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
          |||||||||||||||||||||||||||||||| ||||||||||||||||| ||||| ||| ||
Db    1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT----LDYWGQGTLVT 116
          |||||||||||||||||||||||||| :  |  |||||||||||      ||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK--TGYSSGWGYFDYWGQGTLVT 118

Qy  117 VSS 119
          |||
Db  119 VSS 121
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RESULT 2
S31112
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
R;Reference number: S31104; MUID:92211633; PMID:1730252
A;Accession: S31112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-120 <RAA>
A;Cross-references: EMBL:X62961
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin; immunoglobulin homology <IMM>
F;15-98/Domain: immunoglobulin homology <IMM>

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Query Match             86.7%;  Score 533.5;  DB 2;  Length 120;
Best Local Similarity   88.3%;  Pred. No. 5.9e-43;
Matches 106;  Conservative  0;  Mismatches 13;  Indels  1;  Gaps  1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
       |||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||
Db   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy  61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG-VTGSPTLDYWGQGTLVTVSS 119
       |||||||||||||||||||||||||| ||||||||||
Db  61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATGVVVVVAARDYWGQGTLVTVSS 120
```

RESULT 3
S31117
Ig heavy chain v region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology

```
Best Local Similarity   86.1%;  Pred. No. 6e-43;
Matches 105;  Conservative  1;  Mismatches 13;  Indels  3;  Gaps  1;
```

```
Db 121 SS 122
Qy 118 SS 119
```

RESULT 4
S31679
Ig heavy chain v region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31679
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31679
A;Accession: S31679
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
A;Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID:g30966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

```
Query Match             86.7%;  Score 533;  DB 2;  Length 134;
```

```
Best Local Similarity   88.2%;  Pred. No. 7.3e-43;
Matches 105;  Conservative  1;  Mismatches  9;  Indels  4;  Gaps  1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
       |||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||
Db  20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy  61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
       |||||||||||||||||||||||||| ||||||||||:
Db  80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARBSRG----DYWGQGTLVTVSS 134
```

RESULT 5
P36005
Ig heavy chain v region (M49) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: P36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: P36005
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34026
C;Genetics:
A;Gene: GDB:IGHQ; IGHDY1
A;Cross-references: GDB:1187311; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match             86.5%;  Score 532;  DB 2;  Length 119;
Best Local Similarity   86.6%;  Pred. No. 8e-43;
Matches 103;  Conservative  2;  Mismatches 14;  Indels  0;  Gaps  0;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
       ||||||||||||||||||||||||||||||||    |||||||||||||| |||||| |||
Db   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy  61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
       |||||||||||||||||||||||||| ||||||||||
Db  61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKASDAFDIWGQGTMVTVSS 119
```

RESULT 6
S31603
Ig heavy chain v region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31603
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <CUI>
A;Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>

```
Query Match             86.3%;  Score 531;  DB 2;  Length 132;
Best Local Similarity   88.2%;  Pred. No. 1.1e-42;
Matches 105;  Conservative  1;  Mismatches 11;  Indels  2;  Gaps  1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
       |||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||
```

RESULT 7

Db   16 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 75
Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 119
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   76 ADSVKGRFTISRDNSKNTLYLQMNGLRAEDTAYYYCARDL--FYYFDYWGQGTLVTVSS 132

S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPROT:Q8WUK1
A;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   86.3%; Score 530.5; DB 2; Length 140;
Best Local Similarity 85.8%; Pred. No. 1.3e-42;
Matches 103; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   20 QVQLVESGGGVVQPGSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAPIRYDGSRKYY 79

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG-VTGSPTLDYWGQGTLVTVSS 119
         ||||||||||||||||||||||||| |||| | ||||||||||||||||||||
Db   80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDHIVGATYFDYWGQGTLVTVSS 139

RESULT 8
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:9034957I; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Genetics:
A;Cross-references: UNIPROT:Q8WUK1; GB:M34031
A;Gene: GDB:IGH@; IGHDY1
A;Map position: 14q32.33-14q32.33
A;Cross-references: GDB:118731; OMIM:146910
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   86.0%; Score 529; DB 2; Length 121;
Best Local Similarity 86.8%; Pred. No. 1.6e-42;
Matches 105; Conservative 1; Mismatches 13; Indels 2; Gaps 1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   1 QVQLVESGGGVVQPGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT--GSPTLDYWGQGTLVTVS 118
         |||||||||||||||||||||||||||:: || ||||||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGWALFDYWGQGTLVTVS 120

Qy 119 S 119
         |
Db 121 S 121

RESULT 9
S31116
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
A;Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   85.9%; Score 528.5; DB 2; Length 118;
Best Local Similarity 87.4%; Pred. No. 1.7e-42;
Matches 104; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
         |||||||||||||||||||||||||| ||||| |::||||||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATD-GGKAAPDIWGQGTMVTVSS 118

RESULT 10
S31601
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31601
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31601
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: EMBL:Z14192; NID:g31018; PIDN:CAA78561.1; PID:g31019
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>

Query Match   85.7%; Score 527; DB 2; Length 130;
Best Local Similarity 87.4%; Pred. No. 2.6e-42;
Matches 104; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   16 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 75

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
         :||||||||||||||||||||||||| ||||||::::|||||||||||||||
Db   76 AVSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGL---GFDYWGQGTLVTVSS 130

RESULT 11
S31598
Ig heavy chain V region - human

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31598
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31598
A;Accession: S31585
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <CUI>
C;Cross-references: EMBL:Z14170; NID:g31001; PIDN:CAA78539.1; PID:g31002
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-114/Domain: immunoglobulin homology

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Query Match          85.7%;  Score 527;  DB 2;   Length 135;
Best Local Similarity 87.4%;  Pred. No. 2.7e-42;
Matches   104;  Conservative  0;  Mismatches  15;  Indels   0;  Gaps  0;

Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   17 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 76

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPFLDYWGQGTLVTVSS 119
         |||||||||||||||||||||||||||
Db   77 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKISWEVSRPDYWGQGTLVTVSS 135
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RESULT 12

PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1643
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1643
A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin V region; immunoglobulin homology <IMM>

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Query Match          85.2%;  Score 524;  DB 2;   Length 111;
Best Local Similarity 91.0%;  Pred. No. 4.2e-42;
Matches   101;  Conservative  0;  Mismatches  10;  Indels   0;  Gaps  0;

Qy    9 GGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYYADSVKGRF 68
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRF 60

Qy   69 TISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPFLDYWGQGTLVTVSS 119
         |||||||||||||||||||
Db   61 TISRDNSKNTLYLQMNSLRAEDTAVYYCAKDPLGSRALDYWGQGTLVTVSS 111
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RESULT 13

S46390
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94540092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111

A;Residues: 1-114 <FIG>
C;Cross-references: EMBL:Z31686; NID:g5097802; PIDN:CAA83491.1; PID:g135143
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

RESULT 14

A49028
Ig heavy chain V-III region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
Eur. J. Immunol. 21, 2355-2363, 1991
A;Note: sequence extracted from NCBI backbone (NCBIN:64471, NCBIP:64470)
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Cross-references: GB:S64471; NID:g236904; PIDN:AAB20011.1; PID:g236905
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: A49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-133 <TIM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

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Query Match          85.0%;  Score 522.5;  DB 2;   Length 114;
Best Local Similarity 86.6%;  Pred. No. 5.9e-42;
Matches   103;  Conservative  2;  Mismatches  9;  Indels  5;  Gaps  1;

Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         :||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    1 EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG----VTGSPFLDYWGQGTLVT 116
         ||||||||||||||||||||||||||           :  ||||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRRLIIAAAGNFDYWGQGTLAT 120
```

RESULT 15

S31674
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31674
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31674
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
C;Cross-references: EMBL:Z14204; NID:g30967; PIDN:CAA78573.1; PID:g30968
C;Superfamily: immunoglobulin V region; immunoglobulin homology

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Query Match          84.7%;  Score 521;  DB 2;   Length 133;
Best Local Similarity 82.9%;  Pred. No. 9.6e-42;
Matches   102;  Conservative  3;  Mismatches  14;  Indels  4;  Gaps  1;

Qy    1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWG-----DYWGQGTLVTVSS 114

Qy  117 VSS 119
         |||
Db  121 VSS 123
```

```
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match        84.5%;   Score 519.5;  DB 2;  Length 139;
Best Local Similarity    87.5%;   Pred. No. 1.4e-41;
Matches  105;   Conservative  1;   Mismatches 13;   Indels  1;   Gaps  1;

Qy     1  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY   60
          |||||||||||||||||||||||||||||||||| ||||||||| |||||||||||||||
Db    20  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPCKGLEWVAVISYDGSNKYY   79

Qy    61  ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK-GVTGSPTLDYWGQGTLVTVSS  119
          ||||||||||||||||||||||||||   ||||||||| |:     |||||||||||||
Db    80  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAGLGFFNWFDPWGQGTLVTVSS  139

Search completed: October 13, 2005, 03:11:46
Job time : 25.515 secs
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: October 13, 2005, 02:44:40 ; Search time 122.575 Seconds
                 (without alignments)
                 375.480 Million cell updates/sec

Title: US-10-010-729A-7
Perfect score: 615
Sequence: 1 QVQLVESGGGVVQPGRSLRL...........VTGSPTLDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	611	99.3	119	5	Abb07169	sHigM22 h
2	611	99.3	119	8	Abb07186	sHigM22 h
3	611	99.3	119	8	Adi26654	Human ant
4	544	88.5	123	6	Abr55789	Heavy cha
5	542.5	88.2	254	3	Aay56287	HCAY1 clo
6	542.5	88.2	490	3	Aay56637	hCAY1 bin
7	540.5	87.9	120	6	Ada89174	Human ant
8	540.5	87.9	121	8	Adp47108	Human pho
9	540	87.8	121	8	Adp22284	Human ant
10	539	87.6	119	6	Aae32095	Human VEG
11	538.5	87.6	118	5	Abg30463	Human ant
12	538.5	87.6	241	7	Adg30467	Human GMB
13	538	87.5	117	8	Ado36354	Intracell
14	538	87.5	119	7	Adl91327	VH chain
15	537.5	87.4	583	8	Abm82698	Human dia
16	537	87.3	117	8	Adi22094	Anti-plat
17	537	87.3	121	8	Adp22186	Human ant
18	535.5	87.1	223	2	Aay08598	Anti-huma
19	535	87.0	117	8	Adi22096	Anti-plat
20	535	87.0	244	7	Adg30422	Human GMB
21	535	87.0	519	5	Aau81993	Human sec
22	534.5	86.9	118	5	Aae32097	Human VEG
23	534	86.8	117	8	Adi22095	Anti-plat
24	534	86.8	117	8	Ado36345	Intracell
25	534	86.8	119	7	Adl91318	VH chain

26	532.5	86.6	121	8	Adp47227	Human pho
27	532.5	86.6	223	8	Adl70773	Anti-TNFa
28	532	86.5	119	4	Aau02515	Anti-adip
29	531.5	86.5	116	7	Adc60976	Human ant
30	531.5	86.4	135	7	Adc61032	Human ant
31	531	86.3	119	2	Aar95216	Murine-ex
32	530.5	86.3	126	8	Adp03963	Murine-ex
33	530.5	86.3	252	5	Abp45616	Human Bly
34	530.5	86.3	252	7	Adg96443	Single ch
35	530	86.2	123	8	Adr72700	Human mon
36	530	86.2	123	8	Adr72704	Human mon
37	530	86.2	123	8	Adr72698	Human mon
38	530	86.2	124	8	Adp46956	Murine he
39	530	86.2	472	8	Adr72764	Human mon
40	529.5	86.1	121	8	Adr72221	Human pho
41	529.5	86.1	252	5	Abp45508	Human Bly
42	529.5	86.1	252	7	Adg96335	Single ch
43	529	86.0	115	3	Aab39519	Anti-IL12
44	528.5	85.9	249	5	Abp44501	Human Bly
45	528.5	85.9	249	7	Adg95328	Single ch

ALIGNMENTS

RESULT 1
ABB07169
ID   ABB07169 standard; protein; 119 AA.
XX
AC   ABB07169;
XX
DT   13-MAR-2002 (first entry)
XX
DE   sHigM22 heavy chain variable region clone A sequence.
XX
KW   Neuromodulatory; central nervous system; CNS; sHigM22; LYM 22; AKJR4;
KW   ebvHigM MsI19D10; ebv HigM CB2bG8; CB21E12; CB21E7; MSI19E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS   Homo sapiens.
XX
PN   WO200185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US014902.
XX
PR   10-MAY-2000; 2000US-00568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M, Miller DJ, Pease LR;
XX
DR   WPI; 2002-0665996/09.
DR   N-PSDB; ABA94216.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT   neurite outgrowth, regeneration, remyelination and neuroprotection in
PT   central nervous system, useful to treat post-infectious
PT   encephalomyelitis.
XX
PS   Claim 23; Fig 17; 219pp; English.
XX
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHigM22 (LYM 22), ebvHigM MsI19D10, ebv HigM
CC   CB2bG8, AKJR4, CB21E12, CB21E7 or MSI19E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within

CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture. (I)
CC   is also useful for stimulating remyelination of CNS axons. The antibodies
CC   are useful for preventing infection by a bacterium, virus or like
CC   pathogen that causes demyelination or other neurodegenerative condition
CC   in a subject. Methods where (I) is administered to a patient are useful
CC   for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC   disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC   disease, CNS diseases, and other conditions in the CNS where nerves are
CC   damaged as by trauma. The present sequence represents the sHIgM22 heavy
CC   chain variable region clone A amino acid sequence
SQ   Sequence 119 AA;

Qy   Query Match   99.3%; Score 611; DB 5; Length 119;
     Best Local Similarity   98.3%; Pred. No. 2.7e-49;
Matches 117; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSRKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
           ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLTADTTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119

RESULT 2
ID   ABB07186
AC   ABB07186;
DT   13-MAR-2002 (first entry)
DE   sHIgM22 heavy chain variable region clone B sequence.
KW   Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKCR4;
KW   ebvHIgM MSI19D10; ebv HIgM CB2bG8; CB21B12; CB21E7; MSI19B5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary.
OS   Homo sapiens.
PN   WO20018579? -A1.
PD   15-NOV-2001.
PF   30-MAY-2000; 2000WO-US014902.
PR   10-MAY-2000; 2000US-00568351.
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
PI   Rodriguez M, Miller DJ, Pease LR;
DR   WPI; 2002-066596/09.
DR   N-PSDB; ABA94243.
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT   neurite outgrowth, regeneration, remyelination and neuroprotection in
PT   central nervous system, useful to treat post-infectious
PT   encephalomyelitis.
PS   Claim 23; Fig 17; 219pp; English.
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+

CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHIgM22 (LYM 22), ebvHIgM MSI19D10, ebv HIgM
CC   CB2bG8, AKCR4, CB21B12, CB21E7 or MSI19B5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture. (I)
CC   is also useful for stimulating remyelination of CNS axons. The antibodies
CC   are useful for preventing infection by a bacterium, virus or like
CC   pathogen that causes demyelination or other neurodegenerative condition
CC   in a subject. Methods where (I) is administered to a patient are useful
CC   for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC   disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC   disease, CNS diseases, and other conditions in the CNS where nerves are
CC   damaged as by trauma. The present sequence represents the sHIgM22 heavy
CC   chain variable region clone B amino acid sequence
SQ   Sequence 119 AA;

Qy   Query Match   99.3%; Score 611; DB 5; Length 119;
     Best Local Similarity   98.3%; Pred. No. 2.7e-49;
Matches 117; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSRKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
           ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLTABDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119

RESULT 3
ID   ADI26654
AC   ADI26654;
DT   15-APR-2004 (first entry)
DE   Human anti IgM antibody sHIgM22 VH protein.
KW   Human; antibody; IgM; remyelination; neuronal growth; autoantibody;
KW   demyelination disease; multiple sclerosis; central nervous system; CNS;
KW   axon; glial cell proliferation;
KW   Theiler's murine encephalomyelitis virus infection; CNS injury;
KW   spinal cord injury.
OS   Homo sapiens.
PN   US200318582? -A1.
PD   02-OCT-2003.
PF   13-NOV-2001; 2001US-00010729.
PR   29-APR-1994; 94US-00236520.
PR   08-AUG-1996; 96US-00692084.
PR   07-JAN-1997; 97US-00779784.
PR   28-MAY-1999; 99US-00322862.
PR   30-MAY-2000; 2000US-00580787.
PR   05-DEC-2000; 2000US-00730473.
PA   (MAYO-) MAYO FOUND.
PI   Rodriguez M, Miller DJ, Pease LR;
DR   WPI; 2004-119219/12.

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DR   N-PSDB; AD126655.
XX
PT   New human immunoglobulin M antibody for treating or preventing a
PT   demyelinating disease of the central nervous system in a human or
PT   domestic animal, such as multiple sclerosis.
XX
PS   Claim 7; Fig 35; 159pp; English.
XX
CC   The invention relates to an antibody (I) produced by injecting an
CC   immunocompetent host with an antibody peptide, and harvesting the
CC   antibody, where the peptide comprises a human anti-IgM antibody fragment
CC   given in the specification, or active fragments. Also included are
CC   stimulating administering a monoclonal antibody, or mixtures, in a
CC   mammal (comprising administering a monoclonal antibody, or mixtures,
CC   monomers, active fragments, or recombinant antibodies derived from it,
CC   characterised by their ability to bind structures and cells within the
CC   CNS, including oligodendrocytes), stimulating the proliferation of glial
CC   cells in CNS axons in a mammal (comprising administering a monoclonal
CC   antibody, or mixtures, monomers, active fragments, or recombinant
CC   antibodies derived from it, characterised by their ability to bind
CC   structures and cells within the CNS), treating or preventing a
CC   demyelinating disease of the CNS in a mammal (comprising administering a
CC   monoclonal antibody, or mixtures, monomers, active fragments, or
CC   recombinant antibodies derived from it, characterised by their ability to
CC   bind structures and cells within the CNS, and to stimulate remyelination
CC   of axons of the CNS), stimulating, in vitro, the proliferation of glial
CC   cells from mixed cell culture, stimulating remyelination of CNS axons in
CC   a mammal, a DNA sequence (or degenerate variant of it) which encodes an
CC   antibody(or a peptide analogue, hapten, or active fragment of it, where
CC   the DNA sequence consists of a sequence encoding an anti IgM antibody), a
CC   probe capable of screening for the ability to modulate the production or mimic the
CC   and other agents for the ability to modulate the production or mimic the
CC   activities of mAB sHIgM22, sHIgM46, or combinations of them, a
CC   recombinant virus transformed with recombinant antibody nucleic acids or
CC   vector, imaging a portion of the CNS using the antibody and diagnosing or
CC   monitoring demyelination and/or remyelination of the CNS comprising using
CC   CNS image. The antibody is used to stimulate remyelination of CNS axons,
CC   and to stimulate the proliferation of glial cells in CNS axons,
CC   optionally in vitro. The antibody is used to treat or prevent a
CC   demyelinating disease of the CNS in a human or domestic animal, such as
CC   multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
CC   preferably the mammal is a mouse infected with Strain DA of Theiler's
CC   murine encephalomyelitis virus. The antibody is used to treat a spinal
CC   cord injury and used to screen drugs and other agents for the ability to
CC   modulate the production or mimic the activities of the antibody. The
CC   antibody can be used to image a portion of the CNS which can be used to
CC   diagnose or monitor demyelination and/or remyelination of the CNS. The
CC   present sequence is a variable region of a human anti-IgM antibody (or
CC   fragment).
XX
SQ   Sequence 119 AA;

Query Match             99.3%;  Score 611;  DB 8;  Length 119;
Best Local Similarity   99.2%;
Matches 118;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy      1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSRKYY 60

Qy     61 ADSVKGRFTISRDNSKNTLYLQMNSLTPAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ADSVKGRFTISRDNSKNTLYLQMNSLTPAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119

RESULT 4
ABR55789
ID   ABR55789 standard; protein; 123 AA.
XX
AC   ABR55789;
XX
DT   02-SEP-2003  (first entry)
XX
```

```
DE   Heavy chain variable region of anti-Ang-2 antibody 545 HC.
XX
KW   Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
KW   gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW   angiogenesis; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          26..36
FT                   /note= "complementarity determining region (CDR) 1"
FT   Region          50..66
FT                   /note= "complementarity determining region (CDR) 2"
FT   Region          96..113
FT                   /note= "complementarity determining region (CDR) 3"
XX
XX
PN   WO200030833-A2.
XX
PD   17-APR-2003.
XX
PF   11-OCT-2002; 2002WO-US032613.
XX
PR   11-OCT-2001; 2001US-03286604P.
PR   10-OCT-2002; 2002US-00269805.
XX
PA   (AMGB-) AMGEN INC.
XX
PI   Oliner JD;
XX
DR   WPI; 2003-504963/47.
XX
PT   New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful
PT   for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT   hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
PS   Claim 1; Page 91; 161pp; English.
XX
CC   The invention relates to a specific binding agent, which comprises at
CC   least one peptide selected from any of 62 peptides (ABR55769-830) or its
CC   fragment. The binding agents are antibodies that recognize and bind to
CC   angiopoietin-2 (Ang-2). The specific binding agent, particularly the
CC   antibody, is useful for inhibiting undesired angiogenesis, treating
CC   cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC   2 activity, modulating vascular permeability or plasma leakage, or
CC   treating a disease (e.g. ocular neovascular disease, obesity,
CC   haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
CC   inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC   disease, bone-related disease, or psoriasis) in a mammal. The present
CC   sequence represents a heavy chain variable region of an anti-Ang-2
CC   antibody
XX
SQ   Sequence 123 AA;

Query Match             88.5%;  Score 544;  DB 6;  Length 123;
Best Local Similarity   87.0%;
Matches 107;  Conservative  1;  Mismatches 11;  Indels  4;  Gaps  1;

Qy      1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
          ||||:|||||||||||||||||||||||||||||||   |||||||||||||||||| ||
Db      1 QVQLQESGGGVVQPGRSLRLSCAASGFTFSSSYGHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy     61 ADSVKGRFTISRDNSKNTLYLQMNSLTPAXDTAVYYCAKGVT-----GSPTLDYWGQGTLVT 116
          |||||||||||||||||||||||||||  |||||||||||||     ||||||||||||||
Db     61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGVPDPDYGDYAIDYWGQGTLVT 120

Qy    117 VSS 119
          |||
Db    121 VSS 123

RESULT 5
AAY56287
ID   AAY56287 standard; protein; 254 AA.
```

XX
AC   AAY56287;
XX
DT   08-FEB-2000 (first entry)
XX
DE   HCAT1 clone 25 antibody variable heavy chain protein sequence.
XX
KW   Human cationic amino acid transporter; hCAT1; targeted delivery;
KW   gene delivery; virus-like particle; retroviral envelope molecule;
KW   infection; gene therapy; restenosis; balloon angioplasty;
KW   smooth muscle cell; transduction.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PA   (INTR-) INTROGENE BV.
XX
PR   20-MAY-1998; 98EP-0020169
XX
PN   EP959136-A1.
XX
PD   24-NOV-1999.
XX
PF   20-MAY-1998; 98EP-0020169
XX
PR   20-MAY-1998; 98EP-0020169
XX
DR   WPI; 2000-001283/01.
DR   N-PSDB; AA238770.
XX
PT   New virus-like particle or gene delivery vehicle, useful for gene
PT   therapy.
XX
PS   Claim 13; Fig 16; 66pp; English.
XX
CC   The present invention describes a virus-like particle or gene delivery
CC   vehicle comprising a ligand capable of binding to a human amino acid
CC   transporter. The method is useful for the target delivery of substances
CC   to cells e.g. gene therapy. A human cationic amino acid transporter
CC   (hCAT1) targeted adenovirus is useful for local applications of
CC   adenoviral vector e.g. in patients with restenosis following balloon
CC   angioplasty where smooth muscle cells need to be transduced with an
CC   adenoviral vector carrying the CeNOS cDNA. More efficient transduction of
CC   tissues can be carried out therefore resulting in lower multiplicity's of
CC   infections that can be used and therefore less vector associated toxicity
CC   to the tissues surrounding the target cells. AA238737 to AA238770, and
CC   AAY56264 to AAY56287 represent sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 254 AA;

Query Match   88.2%; Score 542.5; DB 3; Length 254;
Best Local Similarity   87.5%; Pred. No. 1.5e-42;
Matches 105; Conservative   5; Mismatches   9; Indels   1; Gaps   1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||| ||||||||||||||||||||||||||| |||||||||||| |||||||| ||
Db   23 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||:|:|:|: |||||||||| :||||||||||||||
Db   83 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 142

RESULT 6
AAY56637
ID   AAY56637 standard; protein; 490 AA.
XX
AC   AAY56637;
XX
DT   22-FEB-2000 (first entry)
XX
DE   hCAT1 binding human antibody molecule protein sequence.
XX
KW   Virus-like particle; ligand; gene delivery; envelope protein; hCAT1;

XX
KW   human cationic amino acid transporter 1; retrovirus; adenovirus;
KW   targeted delivery; gene therapy; balloon angioplasty.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   EP960942-A2.
XX
PD   01-DEC-1999.
XX
PF   20-MAY-1999; 99EP-0020169
XX
PR   20-MAY-1998; 98EP-0020169
XX
PA   (INTR-) INTROGENE BV.
XX
PT   New gene therapy vectors, useful for treating balloon angioplasty
PT   patients.
XX
DR   WPI; 2000-025491/03.
DR   N-PSDB; AA238921.
XX
PI   Van Es H, Verlinden S, Havenga M;
XX
PS   Claim 13; Fig 16; 50pp; English.
XX
CC   The present invention describes a virus-like particle or gene delivery
CC   vehicle (II) provided with a ligand capable of binding to a human amino
CC   acid transporter. (I) is used to deliver genes to human cells or primate
CC   cells that express the hCAT1 amino acid transporter, such as endothelial,
CC   haematopoietic or smooth muscle cells, as part of a gene therapy regime.
CC   The vectors are especially useful for providing local applications of
CC   adenoviral vector to patients with restenosis following balloon
CC   angioplasty, where smooth muscle cells need to be transduced with CeNOS
CC   cDNA, for example. (I) may also be used to pseudotype recombinant type C
CC   retrovirus including murine leukemia retroviruses and lentiviruses. In
CC   addition (I) may be used in functional genomics where transduction of as
CC   many cell types as possible is required. The new gene delivery vehicles
CC   transduce DNA more efficiently and specifically into tissues that are
CC   hard to transform, such as endothelial cells or smooth muscle cells as
CC   compared to a wildtype adenoviral vector. This increased specificity
CC   results in lower multiplicities of infection which can occur with prior
CC   art vectors, so preventing tissue toxicity. In addition the new vectors
CC   allow DNA to be transduced into cells that are in low abundance in cell
CC   mixtures and tissues, which increases their efficiency for use as gene
CC   therapy vehicles. The alteration of the ligand on the viral envelope
CC   increases the potential host cell range of these vehicles. The present
CC   sequence represents a hCAT1 binding human antibody molecule from the
CC   present invention
XX
SQ   Sequence 490 AA;

Query Match   88.2%; Score 542.5; DB 3; Length 490;
Best Local Similarity   87.5%; Pred. No. 3.1e-42;
Matches 105; Conservative   5; Mismatches   9; Indels   1; Gaps   1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||| ||||||||||||||||||||||||||| |||||||||||| |||||||| ||
Db   259 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 318

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||:|:|:|: |||||||||| :||||||||||||||
Db   319 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 378

RESULT 7
ADA89174
ID   ADA89174 standard; protein; 120 AA.
XX
AC   ADA89174;
XX
DT   20-NOV-2003 (first entry)
XX
DE   hCAT1 binding human antibody molecule protein sequence.

DE   Human antibody 1A9 heavy chain amino acid sequence SEQ ID NO:18.
XX
KW   immunoglobulin; Ig; heavy chain variable domain;
KW   light chain variable domain; major histocompatibility complex; MHC;
KW   gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
XX   cancer.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO200307O752-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003; 2003WO-US005128.
XX
PR   20-FEB-2002; 2002US-0358994P.
XX
PA   (DYAX-) DYAX CORP.
PA   (TECR) TECHNION RES & DEV FOUND LTD.
XX
PI   Hoogenboom HRJM, Reiter Y;
XX
DR   WPI; 2003-663847/62.
DR   N-PSDB; ADA89173.
XX
PT   New protein comprising an immunoglobulin light chain variable (VL) domain
PT   and an immunoglobulin heavy chain variable (VH) domain, useful for
PT   preparing a composition for treating or preventing a cancerous disorder.
XX
PS   Disclosure; Fig 3B; 224pp; English.
XX
CC   The present invention describes a protein comprising an immunoglobulin
CC   (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC   domain. The protein binds a complex comprising a major histocompatibility
CC   complex (MHC) and a peptide, does not substantially bind the MHC in the
CC   absence of the bound peptide, and does not substantially bind the peptide
CC   in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC   MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
CC   comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC   comprising one or more nucleic acids for expressing the Ig that binds a
CC   complex having an MHC and a peptide, does not substantially bind the MHC
CC   in the absence of the bound peptide, and does not substantially bind the
CC   peptide in the absence of the MHC; (3) an isolated nucleic acid
CC   comprising a first segment that encodes the Ig variable domain; (4) a
CC   host cell comprising heterologous nucleic acid sequences that encodes the
CC   novel protein; (5) a transgenic animal whose genome includes heterologous
CC   nucleic acid sequences that encode the protein; (6) identifying the
CC   nucleic acid sequences that encode the protein; (7) expressing
CC   an antigen-binding protein; (8) ablating or killing a target cell that
CC   protein that specifically binds the MHC-peptide complex;
CC   displays a peptide on a surface MHC molecule; (9) treating or preventing
CC   a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC   complex in a sample. A protein of the invention has cytostatic activity,
CC   and can be used in gene therapy. The protein is useful for preparing a
CC   composition for treating or preventing a cancerous disorder. The present
CC   sequence represents the heavy chain of an antibody which binds to an MHC-
CC   peptide complex where the peptide component in as peptide fragment of
CC   gp100.
XX
SQ   Sequence 120 AA;

Query Match   87.9%; Score 540.5; DB 6; Length 120;
Best Local Similarity 88.3%; Pred. No. 1e-42;
Matches 106; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
        |||||| ||||||||||||||||||||||||| ||||||||||||||| ||||||| |||
Db   1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCAKGVGTGSS-PTLDYWGQGTLVTVSS 119
        |||||||||||||||||||||||||||| ||||||||| | |||||||||||||||||
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYGDYALLDYWGQGTLVTVSS 120

RESULT 8
ADP47108
ID   ADP47108 standard; protein; 121 AA.
XX
AC   ADP47108;
XX
DT   09-SEP-2004 (first entry)
XX
DE   Human phospholipase A2-specific monoclonal antibody heavy chain #11.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO200405O850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2002; 2003WO-US038234.
XX
PR   02-DEC-2002; 2002US-0430724P.
XX
PI   Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI   Jia X, Nocerini MR;
XX
DR   WPI; 2004-461119/43.
XX
PT   New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT   useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT   asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS   Claim 1; SEQ ID NO 23; 128pp; English.
XX
CC   The invention comprises a human monoclonal antibody that binds to
CC   phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC   useful in the preparation of a medicament for the treatment of
CC   inflammatory and degenerative disorders stemming from inflammatory
CC   reactions in the joints, skin, and blood vessels, e.g. arthritis, psoriasis,
CC   asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC   amino acid sequence represents the heavy chain from a monoclonal antibody
CC   that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
SQ   Sequence 121 AA;

Query Match   87.9%; Score 540.5; DB 8; Length 121;
Best Local Similarity 87.5%; Pred. No. 1e-42;
Matches 105; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
        |||||| |||||||||||||||||||||||||| ||||||||||||||| ||||| |:|
Db   1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSSYGMHWVRQAPGKGLEWVAAIWYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCAKGVGTGSS-PTLDYWGQGTLVTVSS 119
        |||||||||||||||||||||||||||| ||||||||| | | |:|||||||||:|||||
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGTGTPGAFDIWGQGTMVTVSS 120

RESULT 9
ADP22284
ID   ADP22284 standard; protein; 121 AA.
XX
AC   ADP22284;
XX
DT   09-SEP-2004 (first entry)
XX

DE   Human anti-TNFA antibody heavy chain variable region SEQ ID NO:190.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI   Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI   Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
DR   N-PSDB; ADP22283.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 190; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by selecting the human
CC   monoclonal antibody of (I) and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of a
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostate cancer, or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence represents a human anti-TNFa
CC   antibody heavy chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 121 AA;

Best Local Similarity   87.6%;
Matches 106;   Conservative   2;   Mismatches   11;   Indels   2;   Gaps   1;

Qy   1   QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY   60
       | |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1   QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVIWYDGSNKYY   60

Qy   61   ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVS   118
        |||||||||||||||||||||||||||||||||||:: | ||||:||||||||||||
Db   61   ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARBGDYGGNPYFDYWGQGTLVTVS   120

Qy   119   S   119
        |
Db   121   S   121

RESULT 10
AAB32095
ID   AAB32095 standard; protein; 119 AA.
XX
AC   AAB32095;
XX
DT   24-MAR-2003   (first entry)
XX
DE   Human VEGF-2 hybridoma antibody #1.
XX
KW   Human; vascular endothelial growth factor; VEGF-2; inflammatory disease;
KW   proliferative disorder; tumour; breast; cancer; brain; prostate; colon;
KW   lymphangioma; infection; Kaposi's sarcoma; psoriasis; immunosuppressive;
KW   rheumatoid arthritis; diabetic retinopathy; gene therapy; antimicrobial;
KW   cytostatic; ophthalmological; antibody; autoimmune disease.
XX
OS   Homo sapiens.
XX
PN   WO200283849-A2.
XX
PD   24-OCT-2002.
XX
PF   12-APR-2002; 2002WO-US011404.
XX
PR   13-APR-2001; 2001US-0283391P.
PR   07-SEP-2001; 2001US-0317600P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Albert VR, Ruben SM, Wager RE;
XX
DR   WPI; 2003-093007/08.
DR   N-PSDB; AAD49586.
XX
PS   Disclosure; Page 394; 399pp; English.
XX
CC   The invention relates to vascular endothelial growth factor (VEGF)-2
CC   antibodies. VEGF-2 antibodies are useful for treating, preventing or
CC   ameliorating a disease or disorder, such as inflammatory diseases or
CC   disorders, proliferative disorders, tumours, tumour metastasis, breast
CC   cancer, brain cancer, prostate cancer, colon cancer, lymphangioma, an
CC   infectious disease, Kaposi's sarcoma, an autoimmune disease, rheumatoid
CC   arthritis, psoriasis, diabetic retinopathy, a disease or disorder
CC   associated with aberrant VEGF-2 (receptor) expression, or a disease or
CC   disorder associated with the lack of VEGF-2 (receptor) function. The
CC   antibody is also useful for detecting, diagnosing, prognosing, or
CC   monitoring cancers and other hyperproliferative disorders. VEGF-2 is also
CC   used in gene therapy. The present sequence is human VEGF-2 hybridoma
CC   antibody
XX

New vascular endothelial growth factor (VEGF) - 2 antibodies, for
treating, preventing or ameliorating a disease or disorder, such as
inflammatory diseases, proliferative disorders, autoimmune disorders or
diabetic retinopathy.

RESULT 11
ABG30463

```
SQ   Sequence 119 AA;

Query Match      87.6%;   Score 539;  DB 6;  Length 119;
Best Local Similarity  88.2%;   Pred. No. 1.4e-42;
Matches 105;  Conservative   1;  Mismatches 13;  Indels   0;  Gaps   0;

Qy          1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||||| |||||||||||||||||  |||| |||
Db          1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVALIWDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||||| |||||||||||   |  |||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRABDTAVYYCARDGFGSGCFDYWGQGTLVTVSS 119
```

ID   ABG30463 standard; protein; 118 AA.
XX
AC   ABG30463;
XX
DT   07-OCT-2002 (first entry)
XX
DE   Human anti-CD40 monoclonal antibody 9F7 VH.1 region.
XX
KW   Human; VH.1; heavy chain variable region; CD40; autoimmune disease;
KW   systemic lupus erythematosus; psoriasis; multiple sclerosis;
KW   inflammatory bowel disease; Crohn's disease; rheumatoid arthritis;
KW   organ rejection; lymphoma; non-Hodgkin's lymphoma; monoclonal antibody;
KW   B cell; glycoprotein; proliferation.
XX
OS   Homo sapiens.
XX
PN   WO20228904-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030857.
XX
PR   02-OCT-2000; 2000US-0237556P.
XX
PA   (CHIR) CHIRON CORP.
XX
PI   Chu K, Wang C, Yoshihara C, Donnelly JJ;
XX
DR   WPI; 2002-405169/43.
DR   N-PSDB; ABK88453.
XX
PT   A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT   proliferation, growth or differentiation of a normal human B cells and
PT   lupus erythematosus.
XX
PS   Claim 6; Fig 14; 75pp; English.
XX
CC   The invention relates to a human monoclonal antibody or fragment capable
CC   of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC   on the surface of human B cells), where the antibody or fragment is free
CC   of significant agonistic activity when it binds to the CD40 antigen, and
CC   the growth or differentiation is inhibited. The fragments comprise the
CC   complementarity determining region (CDR) of the light and heavy chains of
CC   the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
CC   2QC4, 12D9, 9F7 and 13B4. Also included are the nucleic acids encoding
CC   the antibody (or fragments). The antibodies or fragments are used for
CC   inhibiting proliferation, growth or differentiation of a normal human B
CC   cells and to inhibit antibody production by B cells. They may also be
CC   useful for treating autoimmune diseases, such as systemic lupus
CC   erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
CC   (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
CC   Hodgkin's Lymphoma). The present sequence represents the antibody 9F7
CC   heavy chain variable region VH.1
XX
SQ   Sequence 118 AA;

RESULT 12
ADG30467

```
Query Match      87.6%;   Score 538.5;  DB 5;  Length 118;
Best Local Similarity  89.9%;   Pred. No. 1.6e-42;
Matches 107;  Conservative   1;  Mismatches 10;  Indels   1;  Gaps   1;

Qy          1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||| ||||||||||||||||||||||||||| ||||||||||||||||  |||| |||
Db          1 QVQLQESGGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSIKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||||  |||||||||||  |  |||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRABDTAVYYCARD-HGSNPLDYWGQGTLVTVSS 118
```

ID   ADG30467 standard; protein; 241 AA.
XX
AC   ADG30467;
XX
DT   26-FEB-2004 (first entry)
XX
DE   Human GMBC683 scFv protein.
XX
KW   GMAD; VH; CDR; complementarity determining region; VL; scFv;
KW   single chain antibody; antidiabetic; type II diabetes; human; GMBC683.
XX
OS   Homo sapiens.
XX
PN   WO200308S093-A2.
XX
PD   16-OCT-2003.
XX
PF   01-APR-2002; 2002US-US009625.
XX
PR   28-MAR-2003; 2003WO-US009625.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Baker KP, Albert VR, Chowdhury P;
XX
DR   WPI; 2003-804305/75.
DR   N-PSDB; ADG30564.
XX
PT   New antibody that specifically binds to GMAD polypeptide, useful for
PT   diagnosing, monitoring, treating, preventing or ameliorating type II
PT   diabetes.
XX
PS   Claim 2; SEQ ID NO 100; 410pp; English.
XX
CC   The invention relates to a novel antibody that specifically binds to a
CC   GMAD polypeptide comprising a first amino acid sequence that is at least
CC   95% identical to a second amino acid sequence of a VH CDR
CC   (complementarity determining region) or VL CDR of an scFv (single chain
CC   antibody molecule). The antibody of the invention demonstrates
CC   antidiabetic activity and may be useful for diagnosing, monitoring,
CC   treating, preventing or ameliorating type II diabetes. The current
CC   sequence is that of the human scFv protein of the invention.
XX
SQ   Sequence 241 AA;

RESULT 13
ID   AD036354 standard; protein; 117 AA.
XX
AC   AD036354;
XX
DT   26-AUG-2004 (first entry)
XX
DE   Intracellular interaction-related scFv protein SeqID18.
XX
KW   immunoglobulin single domain; intracellular environment;
KW   intracellular interaction; immunoglobulin domain; scFv;
KW   single chain variable fragment.
XX
OS   Unidentified.
XX
XX
PN   WO200404185-A2.
XX
PD   03-JUN-2004.
XX
PF   14-NOV-2003; 2003WO-GB004942.
XX
PR   15-NOV-2002; 2002GB-00026729.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Rabbitts TH, Tanaka T;
XX
DR   WPI; 2004-431946/40.
XX
PT   Determining the ability of an immunoglobulin single domain to bind to a
PT   target in an intracellular environment by assessing the intracellular
PT   interaction between the immunoglobulin domain and the target by
PT   monitoring the signal.
XX
PS   Disclosure; SEQ ID NO 18; 66pp; English.
XX
CC   This invention relates to a novel method of determining the ability of an
CC   immunoglobulin single domain to bind to a target in an intracellular
CC   environment comprising assessing the intracellular interaction between
CC   the immunoglobulin domain and the target by monitoring the signal. The
CC   method comprises providing a first molecule and a second molecule, where
CC   stable interaction of the first and second molecules leads to the
CC   generation of a signal; providing a single intracellular immunoglobulin
CC   domain which is associated with the first molecule, where the single
CC   immunoglobulin domain is free of complementary immunoglobulin domains;
CC   providing an intracellular target which is associated with the second
CC   molecule, such that association of the immunoglobulin domain and the
CC   target leads to stable interaction of the first and second molecules and
CC   generation of the signal; and assessing the intracellular interaction
CC   between the immunoglobulin domain and the target by monitoring the
CC   signal. The methods are useful for determining the ability of an
CC   immunoglobulin single domain to bind to a target in an intracellular
CC   environment. The present sequence is that of a single chain variable
CC   fragment (scFv) protein which was used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 117 AA;

Query Match   87.5%; Score 538; DB 8; Length 117;
Best Local Similarity   89.2%;
Matches 107; Conservative   1; Mismatches   8; Indels   4; Gaps   2;

Qy   1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSVISYDGSNKYY 60

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||||||| |||||||||||||| |||| |||||||||
Db   61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK---ASPLHFDYWGQGTLVTVSS 117

RESULT 14
ID   ADL91327 standard; protein; 119 AA.
XX
AC   ADL91327;
XX
DT   20-MAY-2004 (first entry)
XX
DE   VH chain clone A20 of an intracellularly binding immunoglobulin SeqID 18.
XX
KW   antibody; variable chain; cytostatic; cytoplasmic degradation;
KW   intracellular relocation; specific antigen positive cancer; leukaemia;
KW   lymphoma; intracellularly binding immunoglobulin; BCR-ABL.
XX
OS   Unidentified.
XX
XX
PN   WO2003077945-A1.
XX
PD   25-SEP-2003.
XX
PF   14-MAR-2003; 2003WO-GB001077.
XX
PR   14-MAR-2002; 2002GB-00006043.
PR   15-NOV-2002; 2002GB-00026723.
PR   15-NOV-2002; 2002GB-00026727.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Lobato-Caballero MN, Rabbitts TH;
XX
DR   WPI; 2003-779088/73.
XX
PT   Use of an intracellularly binding immunoglobulin comprising at least one
PT   antibody variable chain, in preparing a medicament for degrading one or
PT   more specific antigens, or for treating specific antigen positive cancer,
PT   e.g. leukemia.
XX
PS   Example 1; SEQ ID NO 18; 86pp; English.
XX
CC   This invention relates to novel immunoglobulin molecules that comprise at
CC   least one antibody variable chain VH or VL framework region and are
CC   capable of binding to a specific antigens within an intracellular
CC   environment. Specifically, it refers to antibodies that can form an
CC   insoluble complex with a cognate antigen, such that it can then be target
CC   for degradation via the lysosome or proteosome systems. The present
CC   invention describes the specific target antigen as the oncogenic fusion
CC   protein BCR-ABL or the RAS antigen, such that this method can be used to
CC   prepare a cytostatic medicament for the cytoplasmic degradation or
CC   intracellular relocation of such an antigen for the treatment of the
CC   specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore,
CC   the immunoglobulins may also be used for therapeutic, prophylactic or
CC   diagnostic applications both in vitro and in vivo, as well as for assay
CC   and reagent applications or in functional genomics. This polypeptide
CC   sequence is a variable heavy chain (VH) framework region of an
CC   intracellularly binding anti-ABL antibody of the invention.
XX
SQ   Sequence 119 AA;

Query Match   87.5%; Score 538; DB 7; Length 119;
Best Local Similarity   89.2%;
Matches 107; Conservative   1; Mismatches   8; Indels   4; Gaps   2;

Qy   1 QVQLVESGGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   3 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSVISYDGSNKYY 62

Qy   61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||||||| |||||||||||||| |||| |||||||||
Db   63 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK---ASPLHFDYWGQGTLVTVSS 119

RESULT 15
ABM82698

```
ID   ABM82698 standard; protein; 583 AA.
XX
AC   ABM82698;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID No:2947.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P;
PI   Harthehorne TA, Suchoroleki MT, Altus CM, Pitts SJ, Elder LV;
PI   Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI   Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI   Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI   Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI   Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI   Patury S, Shi X, Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN41350.
XX
PS   Claim 27; Page; 190pp; English.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 583 AA;

Query Match             87.4%;  Score 537.5;  DB 8;  Length 583;
Best Local Similarity   87.7%;  Pred. No. 1.1e-41;
Matches  107;  Conservative   1;  Mismatches   9;  Indels   5;  Gaps   2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKXY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLIFAXDTAVYYCAKGVTGSSPT---LDTWGQGTLVTV 117
              ||||||||||||||||||||||||||| |||||||||||||||| ||   |||||||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDT--PPTCDYFDYWGQGTLVTV 137
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